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OM protein - protein search, using sw model

Run on: January 6, 2006, 21:02:07 ; Search time 46 Seconds

(without alignments)
848.324 Million cell updates/sec

Title: US-10-521-420-1

Perfect score: 2424

Sequence: 1 MKSILGLADTTFTTTDL.....TVKIATVMSVSDTSAEAL 472

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5 COMB.pgp:*
- 2: /cgn2_6/ptodata/1/iaa/6 COMB.pgp:*
- 3: /cgn2_6/ptodata/1/iaa/H COMB.pgp:*
- 4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pgp:*
- 5: /cgn2_6/ptodata/1/iaa/RE COMB.pgp:*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pgp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2407	99.3	472	2	US-09-826-509-469
2	1571.5	64.8	345	1	US-08-118-270-70
3	1571.5	64.8	345	4	PCT-US93-08528-70
4	705	29.1	360	2	US-09-826-509-471
5	365	15.1	393	4	PCT-US96-10618-3
6	364	15.0	364	2	US-09-169-205D-20
7	363	15.0	364	2	US-09-731-030A-15
8	363	15.0	364	2	US-09-811-838-2
9	360	14.9	364	4	PCT-US96-10618-2
10	355	14.6	364	2	US-08-763-938-2
11	353	14.6	381	1	US-08-845-566-3
12	353	14.6	381	1	US-08-467-948A-28
13	353	14.6	381	2	US-08-852-824-18
14	353	14.6	381	2	US-08-467-947A-28
15	353	14.6	381	2	US-09-731-030A-17
16	353	14.6	381	2	US-09-518-383-18
17	353	14.6	381	4	PCT-US96-10618-4
18	352.5	14.5	378	2	US-09-082-088-2
19	352.5	14.5	378	2	US-09-546-117-2
20	351.5	14.5	382	2	US-09-262-477-2
21	349	14.4	470	1	US-08-466-906B-8
22	349	14.4	470	2	US-09-201-746-8
23	346.5	14.3	378	2	US-09-169-205D-22
24	346.5	14.3	378	2	US-09-731-030A-18
25	346	14.3	382	2	US-09-542-733-2
26	344	14.2	382	2	US-09-169-205D-21
27	341	14.1	353	2	US-09-731-030A-16

Sequence 6, Appli	353	2	US-09-811-838-6
Sequence 7861, Ap	359	2	US-09-949-016-7861
Sequence 2, Appli	354	2	US-09-325-897-2
Sequence 2, Appli	354	2	US-09-837-726-2
Sequence 4, Appli	383	1	US-08-196-989B-4
Sequence 4, Appli	383	1	US-08-760-936-4
Sequence 4, Appli	383	2	US-09-225-024-4
Sequence 14, Appli	383	2	US-08-997-803-14
Sequence 4, Appli	384	2	US-08-852-824-4
Sequence 11, Appli	384	2	US-09-731-030A-11
Sequence 13, Appli	384	2	US-09-518-383-4
Sequence 73, Appli	384	2	US-09-731-030A-13
Sequence 73, Appli	334	4	PCT-US93-08528-73
Sequence 2, Appli	351	2	US-08-861-747-2
Sequence 1, Appli	382	2	US-09-274-752D-1
Sequence 2, Appli	351	2	US-08-789-982-2
Sequence 4, Appli	351	2	US-09-811-838-4

ALIGNMENTS

RESULT 1

US-09-826-509-469
; Sequence 469, Application US/09826509
; Patent No. 6806054
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liauw, Chen W.
; TITLE OF INVENTION: No. '6806054' Endogenous Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 469
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-469

Query Match	99.3%	Score 2407;	DB 2;	Length 472;
Best Local Similarity	99.4%	Pred. No. 3.9e-194;		
Matches 469;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
Qy	1	MKSILGLADTTFTTTTDLTYGSDNIQYEDIDKGMASKLGYFPQKPLTSFRGSPQOE	60	
Db	1	MKSILGLADTTFTTTTDLTYGSDNIQYEDIDKGMASKLGYFPQKPLTSFRGSPQOE	60	
Qy	61	KMTAGDNPQLPADQVNITEFYNKSLSFKFENENIOCGENFMDECEFWLNPSQOLAIA	120	
Db	61	KMTAGDNPQLPADQVNITEFYNKSLSFKFENENIOCGENFMDECEFWLNPSQOLAIA	120	
Qy	121	VLSITLGTFTVLENLVLCVILHSRSLRCRPSYHFISGLAVADLLGSVIFYSFIDFHFV	180	
Db	121	VLSITLGTFTVLENLVLCVILHSRSLRCRPSYHFISGLAVADLLGSVIFYSFIDFHFV	180	
Qy	181	HRKDSRNVPFLKGGVTASFTASVGSFLTAIARIYISIHRLAYKRIVTRKAVVAFCIM	240	
Db	181	HRKDSRNVPFLKGGVTASFTASVGSFLTAIARIYISIHRLAYKRIVTRKAVVAFCIM	240	
Qy	241	WTIAIVAVLPILGNCKEKLQSCSDIPPHIDETVLMFWIGVTSVLLPIVYAVYIWLK	300	
Db	241	WTIAIVAVLPILGNCKEKLQSCSDIPPHIDETVLMFWIGVTSVLLPIVYAVYIWLK	300	
Qy	301	AHSHAVRMIRGTQKSIHHTSEDKVQVTRPDQARMAIRLAKTLVLVLIIICWGPLL	360	

Db 301 AHSHAVRMIOQGTOKSIIHTSDGKQVTRPDQARMDIRLAKTLVLILVLIICWGPLL 360
Qy 361 AIMVYDFGKMKLIKTVFAFCSMCLLNSTVNPPIIYALRSKDLRHAFRSMFPCGTAQ 420
Db 361 AIMVYDFGKMKLIKTVFAFCSMCLLNSTVNPPIIYALRSKDLRHAFRSMFPCGTAQ 420
Qy 421 PLDNSMGDSCLHKKHANNAASVHRAAESCIKSTVKIAKVTMSVSTDTSAEAL 472
Db 421 PLDNSMGDSCLHKKHANNAASVHRAAESCIKSTVKIAKVTMSVSTDTSAEAL 472

RESULT 2

US-08-118-270-70
; Sequence 70, Application US/08118270
; Patent No. 5508384
; GENERAL INFORMATION:
; APPLICANT: Murphy, Randall B.
; APPLICANT: Schuster, David I.
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/118,270
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY-2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 345 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-118-270-70

Query Match 64.8%; Score 1571.5; DB 1; Length 345;
Best Local Similarity 90.8%; Pred. No. 4.1e-124;
Matches 324; Conservative 8; Mismatches 12; Indels 13; Gaps 7;
Qy 117 LAIAVLSLT-LGFTTVLENLLVLCVILHSRLCRPSYHFIFGSLAVADLLGVSIFVYSFI 175
Db 1 LAIAVLSLTLLGFTTVLENLLVLCVILHSRLCRPSYHFIFGSLAVADLLGVSIFVYSFV 60
Qy 176 DFHFVHRKDSNVFLFKLGGVTASTASVGSFLTAIARYISIHRLPLAYKRIIVTRPKAVV 235
Db 61 DFHFVHRKDSNVFLFKLGGVTASTASVGSFLTAIDRYISIHPIAYKRIIVRRPKAVV 120
Qy 236 AFCMLMTIAIVIAVLPFLGNCKEKLQSVCSDFPHIDETVLMFWIGTSVLLLFIVYAYM 295
Db 121 AFCIM-TIAIVIAVLPFLGNCKKQSVCCDIFPLIDGTGLMFWIGTSVLLLFIVYAYM 179

Qy 296 YILWKAHSHAVRMIOQGTOKSIIHTSDGKQVTRPDQARMAIRLAKTLVLILVLIIC 355
Db 180 YILWKAHSHAVR-AQGTGQKSIHTSDGKQVTRPDQARMDIRLAKTLVLILVLIIC 238
Qy 356 WGPLAIAMVYDFGKMKLIKTVFAFCSMCLLNSTVNPPIIYALRSKDLRHAFRSMFPC 415
Db 239 WGPLAIAMVYDFG---LLIKTVFAFCSL--LINSVNPPIIYALRSKDLRHAFRS-WPSC 292
Qy 416 EGTAQPLDNSMGDSCLHKKHANNAASVHRAAESCIKSTVKIAKVTMSVSTDTSAEAL 472
Db 293 EGTAQPLDNSMGDSCLHKKHANNTASMHRAESCIKSTVKLA---LVSTDTSAEAL 345

RESULT 3

PCT-US93-08528-70
; Sequence 70, Application PC/TUS9308528
; GENERAL INFORMATION:
; APPLICANT: New York University
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08528
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 345 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US93-08528-70

Query Match 64.8%; Score 1571.5; DB 4; Length 345;
Best Local Similarity 90.8%; Pred. No. 4.1e-124;
Matches 324; Conservative 8; Mismatches 12; Indels 13; Gaps 7;
Qy 117 LAIAVLSLT-LGFTTVLENLLVLCVILHSRLCRPSYHFIFGSLAVADLLGVSIFVYSFI 175
Db 1 LAIAVLSLTLLGFTTVLENLLVLCVILHSRLCRPSYHFIFGSLAVADLLGVSIFVYSFV 60
Qy 176 DFHFVHRKDSNVFLFKLGGVTASTASVGSFLTAIARYISIHRLPLAYKRIIVTRPKAVV 235
Db 61 DFHFVHRKDSNVFLFKLGGVTASTASVGSFLTAIDRYISIHPIAYKRIIVRRPKAVV 120
Qy 236 AFCMLMTIAIVIAVLPFLGNCKEKLQSVCSDFPHIDETVLMFWIGTSVLLLFIVYAYM 295
Db 121 AFCIM-TIAIVIAVLPFLGNCKKQSVCCDIFPLIDGTGLMFWIGTSVLLLFIVYAYM 179
Qy 296 YILWKAHSHAVRMIOQGTOKSIIHTSDGKQVTRPDQARMAIRLAKTLVLILVLIIC 355

Db 180 YILWKAHSHAVR-AQGTQKSIHHTSEDKVQVTRPDQARMDIRLAKTLVLVLVLIIC 238
Qy 356 WGPLLAIMVYDVGKMKLKTIVAFCSMLCLLNSTVNPPIYALRSKDLRHAFRSPSC 415
Db 239 WGPLLAIMVYDVGKMKLKTIVAFCSMLCLLNSTVNPPIYALRSKDLRHAFRSPSC 292
Qy 416 EGTAQPLDMSGSDCLHGHANNAASVHRAESCISKSTVKIAKVTMSVSDTSAEAL 472
Db 293 EGTAQPLDMSGSDCLHGHANNAASVHRAESCISKSTVKIAKVTMSVSDTSAEAL 345

RESULT 4

US-09-826-509-471
; Sequence 471, Application US/09826509
; Patent No. 6806054
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinema, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2001-04-05
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 471
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-471

Query Match 29.1%; Score 705; DB 2; Length 360;
Best Local Similarity 44.8%; Pred. No. 2.7e-51;
Matches 148; Conservative 57; Mismatches 95; Indels 30; Gaps 6;
Qy 78 ITEFYNKSLSPFKNEENIQCGENFMDIECPMVLNPSQOLAIAVLSLTGFTVLENLV 137
Db 6 VTEIANGSKGLDSN-----PKDYMLSGQKTRAVAVLCITLGLLSALENAV 54
Qy 138 LCVILHRSRLCRPSYHFIFGSLAVADLLGSVIFVYSFIDFHFVHRKDSRNVPFLKGGVT 197
Db 55 LYLILSSHQLRRKPSYLFIFGSLAGADFLASVVFACSFVNFHVFHGVDSKAVFLKIGSVT 114
Qy 198 ASFTASVGSPLPTIARIYISIRPLAYKRIUTRPKANVAFCLMWTIAIVIAVPLGWN 257
Db 115 MTFTASVGSLLTATDRYLCLRPSPYKALITRGRALVTGLIMMVLGALVSYLPLMGWTC 174
Qy 258 EKLSQVSDIPPHIDETVLMFWIGVTSVLLFIVVAYMYILWKAHSHAVRMIOGTOKSI 317
Db 175 --CRPCELPFLPNVLLSWLLFIAPFSGIITYGHVWKAHQHVA-----SL 223
Qy 318 IIHTSEDKVQVTRPDQARMA--IRLAKTLVLVLVLIICWGPLLAIMVYDVGKMKLI 375
Db 224 SGH--QDRQV---PGMARMLDVLKKTGLGLVLAVLICFWFVPLMALMAHSLATLSDQV 277
Qy 376 KTVFAFCSMLCLLNSTVNPPIYALRSKDLR 405
Db 278 KKAFAFCSMLCLLNSTVNPPIYALRSGBIR 307

RESULT 5

PCT-US96-10618-3
; Sequence 3, Application PC/TUS9610618
; GENERAL INFORMATION:
; APPLICANT: Coleman, Roger
; APPLICANT: Guegler, Karl J.
; APPLICANT: Au-Young, Janice

; APPLICANT: Bandman, Olga
; APPLICANT: Sellhamer, Jeffrey J.
; TITLE OF INVENTION: A NOVEL HUMAN EDG-2 RECEPTOR HOMOLOG
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10618
; FILING DATE: 20-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/000,352
; FILING DATE: 20-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/567,817
; FILING DATE: 06-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Glaister, Debra J.
; REGISTRATION NUMBER: 33,888
; REFERENCE/DOCKET NUMBER: PF-0042 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 393 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: U18405
; PCT-US96-10618-3

Query Match 15.1%; Score 365; DB 4; Length 393;
Best Local Similarity 27.2%; Pred. No. 1.1e-22;
Matches 109; Conservative 71; Mismatches 176; Indels 44; Gaps 10;
Qy 59 QEKMTAGDNQVLPADQVNITEFYFNKSLSPFKNEENIQCGENFMDIECPMVLNPSQOLA 118
Db 13 QPQFTANNEPQC-----FYNESIAFPYNSGKYLATE-----WNTVSKLV 52
Qy 119 IAVLSLTGFTVLENLVLCVILHRSRLCRPSYHFIFGSLAVADLLGSVIFVYSFIDFH 178
Db 53 MG-LGITVCIFIMLANLVVAVVYVNRHFP-PIYILMANLAAADFFAGLAYFYLMFNTG 110
Qy 179 VFHRKDSRNVPFLKGGVTSFTASVGSPLFTATARIYISIRPLAYKRIUTRPKANVAF 238
Db 111 PNTRRLTVSTWLLRQGLIDTTVTASVANLLAIAIERHITVFRMQLHTRMSNR-RVVVVIV 169
Qy 239 LMWTIAIVIAVPLGLGWNCEKLSQVSDIPPHIDETVLMFWIGVTSVLLFIVVAYMYIL 298
Db 170 VIWTAIVMGAIPIPSVGNWNCIDENCSNMAELYSDSLVFWAIPLNLTFFVWVVLVYAHF 229
Qy 299 WKAHSHAVRMIOGTOKSIHHTSEDKVQVTRPDQARMAIRLAKTLVLVLVLIICWGP 358
Db 230 GYVQRTFMSR-----HSSGPRENRT-----WMSLLKTVIVLGAFLICWTP 273
Qy 359 LLAIMVYDVGKMKLKTIVAFCSMLCLLNSTVNPPIYALRSKDLRHAFRSP--PSCE 416
Db 274 GLVLLLDVCCPQCDVL-AYEKFFLLAEFNSAMNPIIYSYRDKEMSAFTRQILCCQSRSE 332

ORGANISM: Homo sapiens
US-09-811-838-2

Query Match 15.0%; Score 363; DB 2; Length 364;
Best Local Similarity 27.2%; Pred. No. 1.5e-22;
Matches 108; Conservative 72; Mismatches 167; Indels 50; Gaps 10;

QY 59 QERKTAGDNPOLVPADQVNITEFYKSLSSFKENEENIQCGENFMDIECFMVLNPSQOLA 118
DB 13 QPOFTANNEPQC-----FYNESIAFFYNRSGKHLATE-----WNTVSKLV 52
QY 119 IAVLSLTGLTFTVLENLVLCVILHSRLCRPSYHFIGSLAVADLLGVSIFVYSFIDFH 178
DB 53 MG-LGITVCIFIMLANLLVMVAIVVNRPHF-PIYVLMANLAAADPPAGLAYFYLMTGT 110
QY 179 VFHKOSRNVFLFKLGVTASTASVGSFLTAIARIYISIHRLPLAYKRIIVTRPKAVVAF 238
DB 111 PNTRRLTVSTWLLRQGLIDTSLTASVANLLAIAIERHITVFRMQLHTRMSNR-RVVVVIV 169
QY 239 LMWTIAIVIAVPLLGWNCCKLOSCVDIPIPHIDETVLMFWIGVTSVLLLFIVVAYMYIL 298
DB 170 VIWTAIVMGAIFSVGNWNCIDENCSNMAPLYSDSYLVFWAIFNLVTFVVMVLYAHIF 229
QY 299 WKAHSHAVRMIQRGTQKSIITHTSECGKVQVTRPDQARMAIRLAKTILVLIIVLIIWGP 358
DB 230 GYVQRTRMSR-----HSSGPRNRDT-----MMSLLKTVVIVLGFIICTWP 273
QY 359 LLAIMVYDVFQGNKLIKTVPAFCMCLLNSTVNPPIIYALRSKDLRHAFRSMPPSCGT 418
DB 274 GLVLLLDVCCPQCDVL-AYEKFPLLAEFNSAMNPIIYSYRDKEMSATFRQIL-----C 327
QY 419 AQPLDMSMGSDCLHKHANN-----AASVHRAAESCI 450
DB 328 QORSENPTGTESDRSASSLNHTILAGVHSDHVSU 364

RESULT 9

PCT-US96-10618-2
Sequence 2, Application PC/TUS9610618
GENERAL INFORMATION:
APPLICANT: Coleman, Roger
APPLICANT: Guegler, Karl J.
APPLICANT: Au-Young, Janice
APPLICANT: Bandman, Olga
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: A NOVEL HUMAN EDG-2 RECEPTOR HOMOLOG
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10618
FILING DATE: 20-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/000,352
FILING DATE: 20-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/567,817
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Glaister, Debra J.
REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: PP-0042 PCT

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 364 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: Rheumatoid Synovium
CLONE: 80853
PCT-US96-10618-2

Query Match 14.9%; Score 360; DB 4; Length 364;
Best Local Similarity 27.9%; Pred. No. 2.6e-22;
Matches 110; Conservative 70; Mismatches 170; Indels 44; Gaps 11;
QY 59 QERKTAGDNPOLVPADQVNITEFYKSLSSFKENEENIQCGENFMDIECFMVLNPSQOLA 118
DB 13 QPOFTANNEPQC-----FYNESIAFFYNRSGKHLATE-----WNTVSKLV 52
QY 119 IAVLSLTGLTFTVLENLVLCVILHSRLCRPSYHFIGSLAVADLLGVSIFVYSFIDFH 178
DB 53 MG-LGITVCIFIMLANLLVMVAIVVNRPHF-PIYVLMANLAAADPPAGLAYFYLMTGT 110
QY 179 VFHKOSRNVFLFKLGVTASTASVGSFLTAIARIYISIHRLPLAYKRIIVTRPKAVVAF 238
DB 111 PNTRRLTVSTWLLRQGLIDTSLTASVANLLAIAIERHITVFRMQLHTRMSNR-RVVVVIV 169
QY 239 LMWTIAIVIAVPLLGWNCCKLOSCVDIPIPHIDETVLMFWIGVTSVLLLFIVVAYMYIL 298
DB 170 VIWTAIVMGAIFSVGNWNCIDENCSNMAPLYSDSYLVFWAIFNLVTFVVMVLYAHIF 229
QY 299 WKAHSHAVRMIQRGTQKSIITHTSECGKVQVTRPDQARMAIRLAKTILVLIIVLIIWGP 358
DB 230 GYVQRTRMSR-----HSSGPRNRDT-----MMSLLKTVVIVLGFIICTWP 273
QY 359 LLAIMVYDVFQGNKLIKTVPAFCMCLLNSTVNPPIIYALRSKDLRHAFRSMPPSCGT 418
DB 274 GLVLLLDVCCPQCDVL-AYEKFPLLAEFNSAMNPIIYSYRDKEMSATFRQIL-CCORS 331
QY 419 AQPLDMSMGSDCLHKHANN--ASVHRAAESCI 450
DB 332 ENPTAPTEG-SDRSASSLNHTILAGVHSDHVSU 364

RESULT 10

US-08-763-938-2
Sequence 2, Application US/08763938
Patent No. 6140060
GENERAL INFORMATION:
APPLICANT: CHUN, Jerold J.M.
APPLICANT: HECHT, Jonathan H.
TITLE OF INVENTION: CLONED LYSOPHOSPHATIDIC ACID
TITLE OF INVENTION: RECEPTORS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nikaido, Marmelstein, Murray and Oram LLP
STREET: 655 15th Street, N.W., Suite 330 - G St. Lobby
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/763,938

STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,948A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 381 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-467-948A-28

Query Match 14.6%; Score 353; DB 1; Length 381;
Best Local Similarity 27.3%; Pred. No. 1.1e-21;
Matches 102; Conservative 71; Mismatches 129; Indels 72; Gaps 12;

QY 68 POLVP-----ADQVN---ITEFVN---KSLSSFKENEENIQCGNFMFMDIECFMVL 111
DB 3 PTVPLVKAHRSSVDYVNDIIVRHNYTGKLNISADKENSIKL-----47

QY 112 NPSQQLAIAVLSLTGLTFTVLENLVLCVILHSRSLRCRPSYHFIGSLAVADLLGSVIFV 171
DB 48 -----TSVVFILICCFIILENIFVLLTIWTKKPH-RPMYFIGNLSLSDLLAGVAYT 99

QY 172 YSFIDFVHFRKDSRNVPFLKGGVTASFTASVGSFLTAIARYIS-----IHRPLAYKR 226
DB 100 ANLLSGATTYKLTTPAQWFLREGSMFVALSASFSLAIAIERYITMLKMKLHNGSNFR 159

QY 227 IVTRPKAVAFCLMWTIAIVLPLLGWCKEKLQSCSDIFPHIDETYLMEFVIGVTSVL 286
DB 160 LF-----LLISAC--WVLSILGLPIMGWNCISALSSCSVLPYLHKHYILFCTTVFTLL 213

QY 287 LLETV--YAYWYILWKAHSHAVRMIOQTOKSIIHTSDEGKVQVTRPDQARMAIRLAKT 344
DB 214 LLSIVLYCRYSLVTRSRRLTF-----RKNISKASRSSENVALLKT 256

QY 345 LVLIIVLIIICWGLPILAIWYDVGKMKLIKTVF--AFCSMLCLLNSTVNPPIIYALRSK 402
DB 257 VIIVLSVFIACWAPLFIILLDDVGCKV-KTCDILFRAEYFLVLAVLSNGTNPPIIYTLTK 315

QY 403 DLRAFRSMFSPCE 416
DB 316 EMRRAFIRMSCK 329

RESULT 14
US-08-467-947A-28
Sequence 28, Application US/08467947A
Patent No. 6090575
GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: CAO, LIANG
APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPR1
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,947A

;
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04079
; FILING DATE: 30-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-467-947A-28

Query Match 14.6%; Score 353; DB 2; Length 381;
Best Local Similarity 27.3%; Pred. No. 1.1e-21;
Matches 102; Conservative 71; Mismatches 129; Indels 72; Gaps 12;

QY 68 POLVP-----ADQVN---ITEFYN---KSLSSFKENEENIQCGENFMDIECFMVL 111
DB 3 PTVSVLVKAHRSVSDYVNDIIVRHNYVTGKLNISADKENSIKL-----47

QY 112 NPSQQLAIAVLSLTGTFTVLENLLVLCVILHSRLCRPSYHFHIGSLAVADLLGSVIFV 171
DB 48 -----TSVVFILICCFIILENIFVLLTIWTKKPH-RPMYFFIGNLALSOLLAGVAVT 99

QY 172 YSFIDFHVHFKDSRNVLFLKGGVTASTASVGSFLFLTAIARIYS-----IHRPLAYKR 226
DB 100 ANLLLSGATTYKLTTPAQWFLREGSMFVALSASFVSLLAIAIERIYITMLKMKLHNGSNMFR 159

QY 227 IVTRPKAVVAFCLMWTIAIVLPLLGWNCCKLQSCSDIFPHIDETVLMFWIGVTSVL 286
DB 160 LF-----LLISAC--WVLSILGLPLMGWNCISALSSCSTVPLVYHKHYILFCTVFTLL 213

QY 287 LFLFIV--YAYMYILWKAHSHAVRMIOQTQKSIHHTSDGKVQVTRPDQARMALRLAKT 344
DB 214 LLSIVILYCRISLVTRSRRLTF-----RKNISKASRSSENVALLKT 256

QY 345 LVLLILVLLICWGPLLAIWVDYFGKMKLIKTVF--AFCSMLCLLNSTVNPILIIYALRSK 402
DB 257 VIIVLSVFIAFWAPLFIILLDDVGCKV-KTCDILFRAEYFLVLAVLNSGTNPILIIYTLTK 315

QY 403 DLRHAFRSMFPSC 416
DB 316 EMRRAPIRMSCCK 329

RESULT 15
US-09-731-030A-17
; Sequence 17, Application US/09731030A
; Patent No. 6566096
; GENERAL INFORMATION:
; APPLICANT: MUNROE, Donald G
; APPLICANT: GUPTA, Ashwani K.
; APPLICANT: ZASTAWNY, Roman L.
; TITLE OF INVENTION: MAMMALIAN EDG-7 RECEPTOR HOMOLOGS
; FILE REFERENCE: 8074-0015
; CURRENT APPLICATION NUMBER: US/09/731,030A
; CURRENT FILING DATE: 1998-12-29
; PRIOR APPLICATION NUMBER: 60/070,184
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 381
; TYPE: PRT

;
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Mammalian EDG
US-09-731-030A-17

Query Match 14.6%; Score 353; DB 2; Length 381;
Best Local Similarity 27.3%; Pred. No. 1.1e-21;
Matches 102; Conservative 71; Mismatches 129; Indels 72; Gaps 12;

QY 68 POLVP-----ADQVN---ITEFYN---KSLSSFKENEENIQCGENFMDIECFMVL 111
DB 3 PTVSVLVKAHRSVSDYVNDIIVRHNYVTGKLNISADKENSIKL-----47

QY 112 NPSQQLAIAVLSLTGTFTVLENLLVLCVILHSRLCRPSYHFHIGSLAVADLLGSVIFV 171
DB 48 -----TSVVFILICCFIILENIFVLLTIWTKKPH-RPMYFFIGNLALSOLLAGVAVT 99

QY 172 YSFIDFHVHFKDSRNVLFLKGGVTASTASVGSFLFLTAIARIYS-----IHRPLAYKR 226
DB 100 ANLLLSGATTYKLTTPAQWFLREGSMFVALSASFVSLLAIAIERIYITMLKMKLHNGSNMFR 159

QY 227 IVTRPKAVVAFCLMWTIAIVLPLLGWNCCKLQSCSDIFPHIDETVLMFWIGVTSVL 286
DB 160 LF-----LLISAC--WVLSILGLPLMGWNCISALSSCSTVPLVYHKHYILFCTVFTLL 213

QY 287 LFLFIV--YAYMYILWKAHSHAVRMIOQTQKSIHHTSDGKVQVTRPDQARMALRLAKT 344
DB 214 LLSIVILYCRISLVTRSRRLTF-----RKNISKASRSSENVALLKT 256

QY 345 LVLLILVLLICWGPLLAIWVDYFGKMKLIKTVF--AFCSMLCLLNSTVNPILIIYALRSK 402
DB 257 VIIVLSVFIAFWAPLFIILLDDVGCKV-KTCDILFRAEYFLVLAVLNSGTNPILIIYTLTK 315

QY 403 DLRHAFRSMFPSC 416
DB 316 EMRRAPIRMSCCK 329

Search completed: January 6, 2006, 21:13:17
Job time : 48 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 6, 2006, 21:00:32 ; Search time 189 Seconds

(without alignments)
1097.285 Million cell updates/sec

Title: US-10-521-420-1

Perfect score: 2424

Sequence: 1 MKSILDGLADTTRFTTTDL.....TVKIAKVTMSVSDTSAEAL 472

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq 21:*

1: Geneseqp1980s:*

2: Geneseqp1980s:*

3: Geneseqp2000s:*

4: Geneseqp2000s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2424	100.0	472	8	Adh77048 hCB-1 D21
2	2412	99.5	472	2	AAR14196 Human can
3	2412	99.5	472	6	ABF58525 Human can
4	2412	99.5	472	6	ABP81800 Human can
5	2412	99.5	472	7	ADD46383 Human Pro
6	2412	99.5	472	7	ADL15025 Human CB1
7	2412	99.5	472	7	ADN38918 Cancer/an
8	2412	99.5	472	8	ABO60051 Human gen
9	2412	99.5	472	8	ADO29261 Human can
10	2412	99.5	472	9	AEA81221 Human GPC
11	2407	99.3	472	4	ABF56338 Non-endog
12	2401	99.1	472	7	ADN38920 Cancer/an
13	2343.5	96.7	473	2	AAR14195 Rat canna
14	2343.5	96.7	473	7	ADD46381 Rat Prote
15	2340.5	96.6	473	5	ABF57048 Mouse isc
16	2340.5	96.6	473	5	ADO29262 Mouse GPC
17	2209.5	91.2	439	8	ADM82794 Human can
18	2132.5	88.0	789	8	ADU82881 Ligand up
19	1954	80.6	411	7	ADJ70504 Human bea
20	1954	80.6	411	7	ADN38922 Cancer/an
21	1571.5	64.8	345	9	AEA81222 Human can
22	1571.5	64.8	345	2	AAR48749 G-protein
23	1571.5	64.8	345	2	AAW02721 G-protein
24	735.5	30.3	363	8	ADQ97953 Mouse can

25	734.5	30.3	347	8	ADO29264	Ado29264 Mouse GPC
26	710	29.3	360	2	AAR67001	Aar67001 Cannabino
27	710	29.3	360	6	ABP81801	Abp81801 Human can
28	710	29.3	360	6	ABU04877	Abu04877 Human exp
29	710	29.3	360	6	ABU04878	Abu04878 Human exp
30	710	29.3	360	6	ABU04876	Abu04876 Human exp
31	710	29.3	360	6	ABU04875	Abu04875 Human exp
32	710	29.3	360	8	ADO29263	Ado29263 Human GPC
33	709	29.2	360	8	ADQ97956	Adq97956 Human can
34	705	29.1	360	4	ABF56339	Abf56339 Non-endog
35	435	17.9	116	2	AAW03642	Aaw03642 Human can
36	413.5	17.1	180	2	AAR67002	Aar67002 Cannabino
37	410	16.9	80	6	ABP54018	Abp54018 Human cen
38	410	16.9	80	8	ADO28758	Ado28758 Human cen
39	410	16.9	80	8	ADO05262	Ado05262 Central c
40	410	16.9	80	9	ADX44577	Adx44577 Human cla
41	410	16.9	80	9	ADY83813	Ady83813 Central c
42	410	16.9	80	9	AEA13783	Aea13783 Human cen
43	404	16.7	80	5	ABU67237	Abu67237 G-protein
44	369.5	15.2	362	5	ABG75679	Abg75679 Human Edg
45	369.5	15.2	362	8	ADO28787	Ado28787 Arrestin

ALIGNMENTS

RESULT 1

ADH77048
ID ADH77048 standard; protein; 472 AA.

XX AC ADH77048;

XX AC ADH77048;

DT 22-APR-2004 (first entry)

XX hCB-1 D213A double mutant, SEQ ID 1.

XX Anorectic; neuroprotective; cardiovascular; respiratory;

KW gastrointestinal; cannabinoid; CB; receptor; obesity; psychiatric;

KW neurological; immune; cardiovascular; reproductive; endocrine; disorder;

KW respiratory; gastrointestinal; hCB-1 D213A; mutein.

XX Homo sapiens.

OS Synthetic.

XX WO2004008150-A1.

XX 22-JAN-2004.

PD 14-JUL-2003; 2003WO-GB003066.

PF 17-JUL-2002; 2002SE-00002242.

XX (ASTR) ASTRAZENECA AB.

XX (ASTR) ASTRAZENECA UK LTD.

XX Greasley P;

XX WPI; 2004-143121/14.

DR Identifying an inverse agonist of a cannabinoid (CB) receptor, useful in treating obesity, psychiatric and neurological disorders, comprises contacting a test inhibitory agent with constitutively active CB receptor.

XX Claim 31; SEQ ID NO 1; 31pp; English.

PS The invention relates to a method for identifying an inverse agonist of a cannabinoid (CB) receptor comprising contacting a CB receptor test

CC inhibitory agent with the cell expressing the constitutively active CB receptor. The method is useful in identifying an inverse agonist of a CB

CC receptor. The true antagonist or inverse agonist is useful in preparing a medicament for treating or preventing a disorder associated with a CB

CC receptor. The disorder is obesity, psychiatric and neurological

CC disorders. They are also useful in treating immune cardiovascular,
 CC reproductive and endocrine disorders and also diseases related to
 CC respiratory and gastrointestinal systems. The current sequence represents
 CC the amino acid sequence of the hCB-1 D213A double mutant.

XX
 SQ Sequence 472 AA;

Query Match 100.0%; Score 2424; DB 8; Length 472;
 Best Local Similarity 100.0%; Pred. No. 2.2e-241; Indels 0; Gaps 0;
 Matches 472; Conservative 0; Mismatches 0;

QY 1 MKSILDLGLADTTFRITITDLYVGSNDIQYEDIKGDMASKLGYFPQKPLTFRGSPFQE 60
 DB 1 MKSILDLGLADTTFRITITDLYVGSNDIQYEDIKGDMASKLGYFPQKPLTFRGSPFQE 60

QY 61 KMTAGNPQLVPADQVNITEFYNKSLSFKENEENIQCGENFMDIECFMVLNPSQQLATA 120
 DB 61 KMTAGNPQLVPADQVNITEFYNKSLSFKENEENIQCGENFMDIECFMVLNPSQQLATA 120

QY 121 VLSLTGTFVLENLAVLCVILHSRSLRCRPSYHFHIGSLAVADLLGSLVFVYSFIDFHFV 180
 DB 121 VLSLTGTFVLENLAVLCVILHSRSLRCRPSYHFHIGSLAVADLLGSLVFVYSFIDFHFV 180

QY 181 HRKDSRVFLFKLGGVTASFTASVGSLEFLTAARYISIHRLAYKRIIVTRPKAVAFCLM 240
 DB 181 HRKDSRVFLFKLGGVTASFTASVGSLEFLTAARYISIHRLAYKRIIVTRPKAVAFCLM 240

QY 241 WTIAIVAVPLLGWNCCKLQSVCSDFPHIDTYLMFWIGTVSVLLLFIVYAYWYLWK 300
 DB 241 WTIAIVAVPLLGWNCCKLQSVCSDFPHIDTYLMFWIGTVSVLLLFIVYAYWYLWK 300

QY 301 AHSHAVRMIQRTGQKSIITHTSDEGKVQVTRPDQARMAIRLAKTLVLVLLIICWGPLL 360
 DB 301 AHSHAVRMIQRTGQKSIITHTSDEGKVQVTRPDQARMAIRLAKTLVLVLLIICWGPLL 360

QY 361 AIMVYDVFQGNKMLIKTVFAFCMLCLLNSTVNPITIALRSKDLRHAFRSMPPSCBGTQA 420
 DB 361 AIMVYDVFQGNKMLIKTVFAFCMLCLLNSTVNPITIALRSKDLRHAFRSMPPSCBGTQA 420

QY 421 PLDMSGDSCLLKHANNAASVHRAAESCIKSTVKIAKVTMSVSTDTSAEAL 472
 DB 421 PLDMSGDSCLLKHANNAASVHRAAESCIKSTVKIAKVTMSVSTDTSAEAL 472

RESULT 2

AAR14196
 ID AAR14196 standard; protein; 472 AA.

XX
 AC AAR14196;

XX 25-MAR-2003 (revised)

DT 17-DEC-2001 (revised)

DT 19-DEC-1991 (first entry)

XX Human cannabinoid receptor.

XX Cannabis sativa; marijuana; drug test; substance K receptor.

XX Homo sapiens.

XX USN7564075-N.

XX 03-SEP-1991.

XX 08-AUG-1990; 90US-00564075.

XX 08-AUG-1990; 90US-00564075.

XX (USSH) NAT INST OF HEALTH.

PA (USDC) US SEC OF COMMERCE.

XX Matsuda L, Brownstein M;

XX

DR WPI; 1991-303326/41.
 DR N-PSDB; AAQ14003.

XX DNA encoding mammalian cannabinoid receptor - used for producing receptor
 PT for screening drugs and ligands and in detection.

XX
 PS Disclosure; Fig 5; 25pp; English.

XX SKR6 cDNA encoding the rat cannabinoid receptor was isolated from a rat
 CC cerebral cortex cDNA library. An EcoRI-XbaI fragment was used to screen a
 CC human cosmid library. A positive clone was identified and sequenced.
 CC There is ca. 97 per cent homology between this amino acid sequence
 CC deduced from the sequence of the positive human clone and rat cannabinoid
 CC receptor (see AAR14195). Recombinantly produced receptor can be used to
 CC screen for new drugs suitable for treatment of cannabinoid-treatable
 CC conditions, e.g. glaucoma, bronchial asthma, etc. (Note: Revised entry
 CC submitted to correct the patent number format of US Government-owned NDIS
 CC applications to prevent clashes with ongoing US granted patent numbers.
 CC For further information please visit the Derwent web site at
 CC www.derwent.com/dwpi/updates/ntis_us.html.) (Updated on 25-MAR-2003 to
 CC correct PA field.)

XX Sequence 472 AA;

Query Match 99.5%; Score 2412; DB 2; Length 472;
 Best Local Similarity 99.6%; Pred. No. 3.8e-240;
 Matches 470; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKSILDLGLADTTFRITITDLYVGSNDIQYEDIKGDMASKLGYFPQKPLTFRGSPFQE 60
 DB 1 MKSILDLGLADTTFRITITDLYVGSNDIQYEDIKGDMASKLGYFPQKPLTFRGSPFQE 60

QY 61 KMTAGNPQLVPADQVNITEFYNKSLSFKENEENIQCGENFMDIECFMVLNPSQQLATA 120
 DB 61 KMTAGNPQLVPADQVNITEFYNKSLSFKENEENIQCGENFMDIECFMVLNPSQQLATA 120

QY 121 VLSLTGTFVLENLAVLCVILHSRSLRCRPSYHFHIGSLAVADLLGSLVFVYSFIDFHFV 180
 DB 121 VLSLTGTFVLENLAVLCVILHSRSLRCRPSYHFHIGSLAVADLLGSLVFVYSFIDFHFV 180

QY 181 HRKDSRVFLFKLGGVTASFTASVGSLEFLTAARYISIHRLAYKRIIVTRPKAVAFCLM 240
 DB 181 HRKDSRVFLFKLGGVTASFTASVGSLEFLTAARYISIHRLAYKRIIVTRPKAVAFCLM 240

QY 241 WTIAIVAVPLLGWNCCKLQSVCSDFPHIDTYLMFWIGTVSVLLLFIVYAYWYLWK 300
 DB 241 WTIAIVAVPLLGWNCCKLQSVCSDFPHIDTYLMFWIGTVSVLLLFIVYAYWYLWK 300

QY 301 AHSHAVRMIQRTGQKSIITHTSDEGKVQVTRPDQARMAIRLAKTLVLVLLIICWGPLL 360
 DB 301 AHSHAVRMIQRTGQKSIITHTSDEGKVQVTRPDQARMAIRLAKTLVLVLLIICWGPLL 360

QY 361 AIMVYDVFQGNKMLIKTVFAFCMLCLLNSTVNPITIALRSKDLRHAFRSMPPSCBGTQA 420
 DB 361 AIMVYDVFQGNKMLIKTVFAFCMLCLLNSTVNPITIALRSKDLRHAFRSMPPSCBGTQA 420

QY 421 PLDMSGDSCLLKHANNAASVHRAAESCIKSTVKIAKVTMSVSTDTSAEAL 472
 DB 421 PLDMSGDSCLLKHANNAASVHRAAESCIKSTVKIAKVTMSVSTDTSAEAL 472

RESULT 3

ABR58525

ID ABR58525 standard; protein; 472 AA.

XX
 AC ABR58525;

XX 09-JUL-2003 (first entry)

XX Human cannabinoid receptor 1 (brain) protein.

XX Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
 KW heart disease; atherosclerosis; endometriosis.

XX OS Homo sapiens.
XX PN WO2003025138-A2.
XX PD 27-MAR-2003.
XX PF 17-SEP-2002; 2002WO-US029560.
XX PR 17-SEP-2001; 2001US-0323469P.
XX PR 20-SEP-2001; 2001US-0323887P.
XX PR 13-NOV-2001; 2001US-0350666P.
XX PR 08-FEB-2002; 2002US-0355145P.
XX PR 08-FEB-2002; 2002US-0355257P.
XX PR 12-APR-2002; 2002US-0372246P.
XX PA (BOSB-) EOS BIOTECHNOLOGY INC.
XX PI Afar D, Aziz N, Gish KC, Hevesi PA, Mack DH, Wilson KE;
PI Zlotnik A;
XX WPI; 2003-354600/33.
XX N-PSDB; ACC72645.
XX New genes that are up-regulated or down-regulated in cancers, useful as
PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
PT therapeutic targets for screening drugs for treating these diseases.
XX Claim 12; Page 143; 767pp; English.
XX The present invention describes an isolated nucleic acid molecule, which
CC comprises the sequence of any of the genes that are up-regulated or down-
CC regulated in specific cancers (e.g. about 1031 genes up-regulated in
CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
CC related gene nucleotide sequences which encode the proteins given in
CC ABR58521 to ABR58709. Also described: (1) determining the presence or
CC absence of a pathological cell in a patient; (2) an expression vector
CC comprising a nucleic acid molecule described above; (3) a host cell
CC comprising the vector; (4) an isolated polypeptide, which is encoded by
CC the nucleic acid; (5) an antibody that specifically binds the polypeptide
CC of (4); (6) specifically targeting a compound to a pathological cell in a
CC patient by administering to the patient the antibody above; and (7) a
CC drug screening assay. The nucleic acid is useful as diagnostic markers or
CC therapeutic targets. In particular, the nucleic acid is useful for
CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
CC atherosclerosis and endometriosis. The nucleic acid is also useful in
CC drug screening, particularly for identifying agents for treating these
XX pathologies
XX Sequence 472 AA;
Query Match 99.5%; Score 2412; DB 6; Length 472;
Best Local Similarity 99.6%; Pred. No. 3.8e-240;
Matches 470; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1 MKSILDGLADTFFRTITDLYVGSNDIQYEDIKGMASKLGYFPQKPLTSFRGSPQ 60
Db 1 MKSILDGLADTFFRTITDLYVGSNDIQYEDIKGMASKLGYFPQKPLTSFRGSPQ 60
Oy 61 KMTAGDNPOLPADQVNITEFYNKLSLFFKNEENIQCGENFMDECFLVNLNPSQOLAIA 120
Db 61 KMTAGDNPOLPADQVNITEFYNKLSLFFKNEENIQCGENFMDECFLVNLNPSQOLAIA 120
Oy 121 VLSLTGTFVLENLVLCVILHSRLCRPSYHPIGSLAVADLIGSVIFVYSFIDHFVF 180
Db 121 VLSLTGTFVLENLVLCVILHSRLCRPSYHPIGSLAVADLIGSVIFVYSFIDHFVF 180
Oy 181 HRKDSRNVPFLKGGVGTASVGSLSFLTAIYRISIRHPLAYKRIYTRPKAVVAFCLM 240
Db 181 HRKDSRNVPFLKGGVGTASVGSLSFLTAIYRISIRHPLAYKRIYTRPKAVVAFCLM 240

Oy 241 WTIAIVIAVLPLLGWNCCKLQSVCSDFPHIDETYLMEFVIGVTSVLLLFVIYAYMYLWK 300
Db WTIAIVIAVLPLLGWNCCKLQSVCSDFPHIDETYLMEFVIGVTSVLLLFVIYAYMYLWK 300
Oy 301 AHSNAVMTQRTGQKSIITHTSEDGKVQVTRPQDQARMAIRLAKTLVLVLLVLIICWGP 360
Db AHSNAVMTQRTGQKSIITHTSEDGKVQVTRPQDQARMDIRLAKTLVLVLLVLIICWGP 360
Oy 361 AINVDVDFGKWKLIKTVFAFCSCMLCLLNSTVNPPIIYALSKDLRHAFRSMFSPCECTAQ 420
Db AINVDVDFGKWKLIKTVFAFCSCMLCLLNSTVNPPIIYALSKDLRHAFRSMFSPCECTAQ 420
Oy 421 PLDSMGDSCLLHKHANNAAASVHRAABSCIKSTVKIAKVTMSVSTDTSAAL 472
Db PLDSMGDSCLLHKHANNAAASVHRAABSCIKSTVKIAKVTMSVSTDTSAAL 472
RESULT 4
ABP81800
ID ABP81800 standard; protein; 472 AA.
XX AC ABP81800;
XX DT 04-MAR-2003 (first entry)
XX DE Human cannabinoid receptor 1 protein SEQ ID NO:84.
XX KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
ulcer.
XX KW Homo sapiens.
XX WO200261087-A2.
XX 08-AUG-2002.
XX 19-DEC-2001; 2001WO-US050107.
XX 19-DEC-2000; 2000US-0257144P.
XX (LIFE-) LIFESPAN BIOSCIENCES INC.
XX Burmer GC, Roush CL, Brown JP;
XX WPI; 2003-046718/04.
XX N-PSDB; ABZ42646.
XX New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.
XX Disclosure; Fig 1; 523pp; English.
XX The present invention describes antigenic peptides (I) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (1) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for

CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, or
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention
XX
SQ Sequence 472 AA;
Query Match 99.5%; Score 2412; DB 6; Length 472;
Best Local Similarity 99.6%; Pred. No. 3.8e-240;
Matches 470; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MKSILDGLADTTFRITTTDLLVYGSNDIQYEDIKGDMASKLGYFPQKFLTSFRGSPFOE 60
DB |||
QY 1 MKSILDGLADTTFRITTTDLLVYGSNDIQYEDIKGDMASKLGYFPQKFLTSFRGSPFOE 60
DB |||
QY 61 KMTAGNPOLVPADQVNITEFYNKSLSPKENEENIQCGENFMDIECFVNLNPSQOLA 120
DB |||
QY 61 KMTAGNPOLVPADQVNITEFYNKSLSPKENEENIQCGENFMDIECFVNLNPSQOLA 120
DB |||
QY 121 VLSLTGTTFTVLENLVLCVILHSRLCRPSVHFTGSLAVADLLGSLVFVYSFIDFHFV 180
DB |||
QY 121 VLSLTGTTFTVLENLVLCVILHSRLCRPSVHFTGSLAVADLLGSLVFVYSFIDFHFV 180
DB |||
QY 181 HRKDSRNVELFKLGGVTSFTASVGSFLTAIARYISIHRLAYKRIIVTRPKAVAFCLM 240
DB |||
QY 181 HRKDSRNVELFKLGGVTSFTASVGSFLTAIARYISIHRLAYKRIIVTRPKAVAFCLM 240
DB |||
QY 241 WTIAIVAVPLLGNCEKLSQVCSDFPHIDETVLMFWIGTSLVLLFVIVAYMVLWK 300
DB |||
QY 241 WTIAIVAVPLLGNCEKLSQVCSDFPHIDETVLMFWIGTSLVLLFVIVAYMVLWK 300
DB |||
QY 301 AHSNAVMTQRGQTSIIHTSDGKVQVTRPDQARMALRLAKTLVLVLIIICWGPLL 360
DB |||
QY 301 AHSNAVMTQRGQTSIIHTSDGKVQVTRPDQARMALRLAKTLVLVLIIICWGPLL 360
DB |||
QY 361 AIMVYDVFQGMNKLITVFQFCSMLCLNLTSTNPIIYALRSKDLRHAFRSMFPCBGTQA 420
DB |||
QY 361 AIMVYDVFQGMNKLITVFQFCSMLCLNLTSTNPIIYALRSKDLRHAFRSMFPCBGTQA 420
DB |||
QY 421 PLDNSMGDSCLHGHANNAASVHRAAESCTKSTVKIAKVTMSVSTDTSAEL 472
DB |||
QY 421 PLDNSMGDSCLHGHANNAASVHRAAESCTKSTVKIAKVTMSVSTDTSAEL 472
DB |||

RESULT 5

ADD46383

ID ADD46383 standard; protein; 472 AA.

XX

XX

XX

29-JAN-2004 (first entry)

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
PA
PI Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
DR GENBANK; P21554.
XX
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 472 AA;

Query Match 99.5%; Score 2412; DB 7; Length 472;

Best Local Similarity 99.6%; Pred. No. 3.8e-240; Mismatches 2; Indels 0; Gaps 0;

Matches 470; Conservative 0;

QY 1 MKSILDGLADTTFRITTTDLLVYGSNDIQYEDIKGDMASKLGYFPQKFLTSFRGSPFOE 60
DB |||
QY 1 MKSILDGLADTTFRITTTDLLVYGSNDIQYEDIKGDMASKLGYFPQKFLTSFRGSPFOE 60
DB |||
QY 61 KMTAGNPOLVPADQVNITEFYNKSLSPKENEENIQCGENFMDIECFVNLNPSQOLA 120
DB |||
QY 61 KMTAGNPOLVPADQVNITEFYNKSLSPKENEENIQCGENFMDIECFVNLNPSQOLA 120
DB |||
QY 121 VLSLTGTTFTVLENLVLCVILHSRLCRPSVHFTGSLAVADLLGSLVFVYSFIDFHFV 180
DB |||
QY 121 VLSLTGTTFTVLENLVLCVILHSRLCRPSVHFTGSLAVADLLGSLVFVYSFIDFHFV 180
DB |||
QY 181 HRKDSRNVELFKLGGVTSFTASVGSFLTAIARYISIHRLAYKRIIVTRPKAVAFCLM 240
DB |||
QY 181 HRKDSRNVELFKLGGVTSFTASVGSFLTAIARYISIHRLAYKRIIVTRPKAVAFCLM 240
DB |||
QY 241 WTIAIVAVPLLGNCEKLSQVCSDFPHIDETVLMFWIGTSLVLLFVIVAYMVLWK 300
DB |||

Db	241	WTIAIVAVLPLLGWNCCKLQSVCSDFPHIDETYLFWIGVTSVLLFVIYAYMYLWK	300
Qy	301	AHSHAVRMIOGRTQKSIHHTSEDKVQVTRPDQARMAIRLAKTLVLVLVLIICWGPIL	360
Db	301	AHSHAVRMIOGRTQKSIHHTSEDKVQVTRPDQARMDIRLAKTLVLVLVLIICWGPIL	360
Qy	361	AIWYDVFGKWNKLIKTVFAFCMCLLNSTVNPPIIYALRSKDLRHAFRSMFSCGTAQ	420
Db	361	AIWYDVFGKWNKLIKTVFAFCMCLLNSTVNPPIIYALRSKDLRHAFRSMFSCGTAQ	420
Qy	421	PLDNMGSDSCLHGHANNAASVHRAESCIKSTVKIAKVTMSVSTDTSAEAL	472
Db	421	PLDNMGSDSCLHGHANNAASVHRAESCIKSTVKIAKVTMSVSTDTSAEAL	472
RESULT 6			
ID	ADL15025	standard; protein; 472 AA.	
XX	ADL15025;		
AC	ADL15025;		
DT	06-MAY-2004	(first entry)	
DE	Human CB1 cannabinoid receptor protein for cancer treatment.		
KW	cytostatic; gene therapy; binding moiety; medicine; imaging; diagnosis;		
KW	prognosis; mantle cell lymphoma; cancer.		
OS	Homo sapiens.		
XX	WO2003068268-A2.		
XX	21-AUG-2003.		
XX	13-FEB-2003;	2003WO-EP001461.	
XX	14-FEB-2002;	2002GB-00003480.	
PR	29-JUN-2002;	2002GB-00015095.	
XX	(BIOI-) BIOINVENT INT AB.		
XX	Ek S, Borrebaeck CAK, Ehinger M;		
XX	WPI; 2003-697496/66.		
DR	N-PSDB; ADL15026.		
XX	New compound for treating, imaging, diagnosing or prognosing mantle cell		
PT	lymphoma, comprises a binding moiety (e.g. antibody) that binds to a		
PT	protein (e.g. human autotoxin polypeptide), and a further moiety (e.g.		
PT	nucleic acid).		
XX	Disclosure; SEQ ID NO 37; 342pp; English.		
XX	The invention relates to a compound comprising a binding moiety which		
CC	selectively binds to a protein or polypeptide listed in the specification		
CC	(e.g. human autotoxin polypeptide or human CD24 signal transducer		
CC	polypeptide), and a further moiety. The compound is useful in medicine or		
CC	in the treatment, imaging, diagnosis or prognosis of mantle cell		
CC	lymphomas (MCL). It is used in preparing a medicament for treating MCL, a		
CC	diagnostic or prognostic agent for MCL, or an agent for imaging MCL cells		
CC	in the body of an individual. This sequence corresponds to one of the		
CC	polypeptides of the invention.		
XX	Sequence 472 AA;		
Qy	Query Match	99.5%; Score 2412; DB 7; Length 472;	
Best	Local Similarity	99.6%; Pred. No. 3.8e-240;	
Matches	470; Conservative	0; Mismatches 2; Indels 0; Gaps 0;	
Qy	1	MKSILDGLADTTFRITTDLLVGSNDIQYEDIKGMASKLGYFPQKFLTSFRGSPFQE	60
Db	1	MKSILDGLADTTFRITTDLLVGSNDIQYEDIKGMASKLGYFPQKFLTSFRGSPFQE	60

XX (EOSB-) EOS BIOTECHNOLOGY INC.
PI Afar D, Aziz N, Gineburg WM, Gish KC, Glynn R, Hevezi PA;
PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX WPI; 2003-468649/44.
DR N-PSDB; ADN38917.
XX
XX Determining the presence or absence of a pathological cell in a patient,
PT useful for diagnosing, prognosing or treating cancer, comprises detecting
PT a nucleic acid in a biological sample.
XX
XX Claim 12; SEQ ID NO 236; 1385pp; English.
XX
XX The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC whose expression is upregulated or downregulated in specific cancers or
CC other diseases such as angiogenic or fibrotic disorders, and to methods
CC of determining the presence or absence of a pathological cell in a
CC patient by detecting a nucleic acid at least 80% identical to those of
CC the invention or by detecting a polypeptide of the invention. The
CC invention also relates to expression vectors and host cells comprising a
CC nucleic acid of the invention; antibodies which specifically bind a
CC polypeptide of the invention; use of such antibodies for drug targeting;
CC and methods of screening for modulators of activity or expression of the
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC antibodies and methods are useful for diagnosing, prognosing and treating
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC neovascularisation syndromes, scarring and uterine fibroids. They may
CC also be useful in wound healing and in contraception. The present
CC sequence represents a polypeptide of the invention.
XX
XX Sequence 472 AA;

Query Match 99.5%; Score 2412; DB 7; Length 472;
Best Local Similarity 99.6%; Pred. No. 3.8e-240;
Matches 470; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MXSILDLGADTTTPTITDLYVGSNDIQVEDIKGDMASKLGVFPQKPLTSPRGSPFOE 60
DB 1 MXSILDLGADTTTPTITDLYVGSNDIQVEDIKGDMASKLGVFPQKPLTSPRGSPFOE 60
QY 61 KMTAGNPOLVPADQVNITEFYNKSLSFFKNEENIQCCGFNFMDIECFWVLPNPSQQLATA 120
DB 61 KMTAGNPOLVPADQVNITEFYNKSLSFFKNEENIQCCGFNFMDIECFWVLPNPSQQLATA 120
QY 121 VLSLTGLTFTVLENLVLVILHSRLCRPSYHFTIGSLAVADLLGSLVIFVYSFIDFHV 180
DB 121 VLSLTGLTFTVLENLVLVILHSRLCRPSYHFTIGSLAVADLLGSLVIFVYSFIDFHV 180
QY 181 HRKDSRNVLFLKGGVTASVLSLFTATARYISIHRLPLAYKEIVTRPKAVAFCLM 240
DB 181 HRKDSRNVLFLKGGVTASVLSLFTATARYISIHRLPLAYKEIVTRPKAVAFCLM 240
QY 241 WTIAIVAVPLLGWCKEKLQSCDSIFPHIDETLMFWIGTVSLLPLFTVAYMYILNK 300
DB 241 WTIAIVAVPLLGWCKEKLQSCDSIFPHIDETLMFWIGTVSLLPLFTVAYMYILNK 300
QY 301 AHSHAVRMIQRGQTKSIITHTSDGKVQVTRPDQARMALRLAKTLVLVLVLIICWGPLL 360
DB 301 AHSHAVRMIQRGQTKSIITHTSDGKVQVTRPDQARMALRLAKTLVLVLVLIICWGPLL 360
QY 361 AIMVYDFGQWNLKITVFAFCMCLNLTNPIIYALRSKDLRHFSPMPCSGTAQ 420
DB 361 AIMVYDFGQWNLKITVFAFCMCLNLTNPIIYALRSKDLRHFSPMPCSGTAQ 420
QY 421 PLDNSMGDSCLHKKHANNAASVHRAAESCIKSTVKIAKVTMSVSTDTSAEAL 472
DB 421 PLDNSMGDSCLHKKHANNAASVHRAAESCIKSTVKIAKVTMSVSTDTSAEAL 472

ABO60051
ID ABO60051 standard; protein; 472 AA.
XX
AC ABO60051;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human genome derived single exon protein #6285.
XX
KW Human; gene expression; single exon probe; microarray;
KW alternative splicing event; genomic alteration.
XX
OS Homo sapiens.
XX
PN US2003194704-A1.
XX
PD 16-OCT-2003.
XX
PF 03-APR-2002; 2002US-00029386.
XX
PR 03-APR-2002; 2002US-00029386.
XX
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
XX
PI Penn SG, Rank DR, Hanzel DK;
XX
DR WPI; 2004-119264/12.
XX
PT New human genome-derived single exon nucleic acid probes useful for human
PT gene expression analysis, for identifying or characterizing alternative
PT splicing events, for assessing genomic alterations or as tools for
PT surveying tissues.
XX
PS Claim 45; SEQ ID NO 33685; 80pp; English.
XX
CC The invention relates to a nucleic acid probe for measuring human gene
CC expression, comprising any of the 27,400 fully defined nucleotide
CC sequences in the specification, or their complements or fragments, and
CC encoding at least 8 amino acids of any of the 688 amino acid sequences
CC fully defined in the specification. The probe is a single exon probe that
CC hybridises under high stringency conditions to a nucleic acid molecule
CC expressed in human cells or tissues. Also included are a spatially-
CC addressable set of single exon nucleic acid probes for measuring human
CC gene expression comprising a plurality of single exon nucleic acid
CC probes cited above, where each of the plurality of probes is separately
CC and addressably isolatable or amplifiable from the plurality), a single
CC exon microarray for measuring human gene expression, a method of
CC measuring human gene expression, a vector comprising the single exon
CC probe cited above, an ORF-encoded peptide comprising at least 8
CC contiguous amino acids of any of the above-mentioned amino acid
CC sequences (optionally with conservative amino acid substitutions), an
CC isolated antibody that binds specifically to a peptide cited above,
CC methods of selling and/or licensing single exon probes or microarrays to
CC a customer desiring to measure gene expression, a method of providing
CC human gene expression data by subexpression, and a computer-readable
CC storage medium which contains a database having a plurality of records
CC (each record including data on the expression of a single exon probe
CC cited above. The probe, methods and apparatus are useful in gene
CC expression analysis. The probes may be used as tools for surveying
CC tissues to detect the presence of expressed messages that contain their
CC specific exon, or in constructing genome-derived single exon microarrays.
CC In addition, the probes are used in identifying and characterising
CC alternative splicing events, in detecting and characterising gross
CC alterations in the genomic locus that includes their exon, in assessing
CC smaller genomic alterations, in priming the synthesis of nucleic acids,
CC or in expressing the ORF-encoded peptide. The present sequence is a human
CC single exon probe protein of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO DocID=20030194704
CC seqdata.uspto.gov/sequence.html?DocID=20030194704
XX

SQ Sequence 472 AA;
Query Match 99.5%; Score 2412; DB 8; Length 472;
Best Local Similarity 99.6%; Pred. No. 3.8e-240; Indels 0; Gaps 0;
Matches 470; Conservative 0; Mismatches 2;

Qy 1 MKSLDGLADTTFTTTTDLVYGSNDIQVEDIKGDWASKLGYFPQKPLTSFRGSPFQE 60
Db 1 MKSLDGLADTTFTTTTDLVYGSNDIQVEDIKGDWASKLGYFPQKPLTSFRGSPFQE 60

Qy 61 KMTAGDNPQLVPADQVNITEFYKSLSSFKENEENIQCGENFMDEICFVNLNPSQOLAIA 120
Db 61 KMTAGDNPQLVPADQVNITEFYKSLSSFKENEENIQCGENFMDEICFVNLNPSQOLAIA 120

Qy 121 VLSLTGLTFTVLENLVLCVILHSRSLRCRPSYHFHIGSLAVADLLGSVIFYSFIDFHFV 180
Db 121 VLSLTGLTFTVLENLVLCVILHSRSLRCRPSYHFHIGSLAVADLLGSVIFYSFIDFHFV 180

Qy 181 HRKDSRNVLFPKLGWVTASFTASVGSFLFLTAIARYISIHRLAYKRIVTRPKAVVAFCLM 240
Db 181 HRKDSRNVLFPKLGWVTASFTASVGSFLFLTAIARYISIHRLAYKRIVTRPKAVVAFCLM 240

Qy 241 WTIAIVAVLPLLGWNCCKLQSCSDIFPHIDETFLMFWIGTSLVLLFIYAYMYILWK 300
Db 241 WTIAIVAVLPLLGWNCCKLQSCSDIFPHIDETFLMFWIGTSLVLLFIYAYMYILWK 300

Qy 301 AHSNAVMIQRTGKSIITHTSEBGKQVQVTRPDQARMAIRLAKTLVLLVLLICWGPILL 360
Db 301 AHSNAVMIQRTGKSIITHTSEBGKQVQVTRPDQARMDIRLAKTLVLLVLLICWGPILL 360

Qy 361 AIMYVDVFGKMKLIKTVFPCSMCLLNSVNPVILVALRSKDLRHAFRSPFCEGTQAQ 420
Db 361 AIMYVDVFGKMKLIKTVFPCSMCLLNSVNPVILVALRSKDLRHAFRSPFCEGTQAQ 420

Qy 421 PLDMSMGDSDCLEHANNAAVHRAESCIKSTVKIAKVTMSVSTDTSAEAL 472
Db 421 PLDMSMGDSDCLEHANNAAVHRAESCIKSTVKIAKVTMSVSTDTSAEAL 472

RESULT 9
ADO29261
XX ID ADO29261 standard; protein; 472 AA.
AC ADO29261;
XX
XX
XX 29-JUL-2004 (first entry)
XX
XX Human GPCR CNR1, SEQ ID NO:362.
XX
XX G protein-coupled receptor; GPCR; drug screening; diagnosis;
KW transgenic mouse; neurological disorder; adrenal gland disorder;
KW colon disorder; intestinal disorder; cardiovascular disorder;
KW muscular disorder; blood disorder; immune disorder; bone disorder;
KW joint disorder; metabolic disorder; nutritive disorder; cancer;
KW kidney disorder; liver disorder; lung disorder; breast disorder;
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;
KW cytotatic; antiinflammatory; vasotropic; antiangular; antiarhythmic;
KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
KW virucide; hepatotropic; antibacterial; antianemic; antiseborrhoeic;
KW dermatological; antitumor; antithyroid; antiallergic; anorectic;
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
KW receptor.
XX
XX Homo sapiens.
OS
XX
XX WO2004040000-A2.
XX
XX 13-MAY-2004.
XX
XX
XX 09-SEP-2003; 2003WO-US028226.
XX

PR 09-SEP-2002; 2002US-0409303P.
XX 09-APR-2003; 2003US-0461329P.
PA (PRIM-) PRIMAL INC.
XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
PI Madisen L, McIlwain KL, Pavlova MN, Vassiliadis D, Zeng H;
XX WPI; 2004-390329/36.
DR N-PSDB; ADO29849.
XX
XX Novel mammalian G protein coupled receptors, useful for identifying
PT compounds that modulates diagnosing and treating disease condition
PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
PT pectoris, Parkinson's disease.
XX
XX Claim 151; SEQ ID NO 362; 542pp; English.
XX
XX The invention relates to human and mouse G protein-coupled receptors
CC (GPCRs) and nucleic acids encoding them. The invention also relates to
CC sequences at least 90% identical to the GPCR proteins and nucleic acids
CC of the invention; methods of treating, preventing or diagnosing diseases
CC associated with GPCRs of the invention; methods of screening for
CC compounds useful in the treatment of GPCR-related diseases; a transgenic
CC mouse comprising a GPCR gene of the invention; a mouse comprising a
CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
CC from the transgenic mice; kits comprising several mice, each of which has
CC a mutation in a different GPCR gene of the invention; and kits comprising
CC probes which hybridise to GPCR polynucleotides of the invention. The
CC invention further discloses variants of the GPCR polypeptides and vectors
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
CC be used in the diagnosis, treatment or prevention of a wide variety of
CC diseases including neurological disorders (e.g., Alzheimer's disease,
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
CC disorders of the adrenal gland; disorders of the colon or intestine
CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
CC myocardial infarction); muscular disorders (e.g., autoimmune disorders or
CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
CC invention. Note: The full sequence data for this patent did not form part
CC of the printed specification; those sequences not shown were obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 472 AA;
Query Match 99.5%; Score 2412; DB 8; Length 472;
Best Local Similarity 99.6%; Pred. No. 3.8e-240; Indels 0; Gaps 0;
Matches 470; Conservative 0; Mismatches 2;

Qy 1 MKSLDGLADTTFTTTTDLVYGSNDIQVEDIKGDWASKLGYFPQKPLTSFRGSPFQE 60
Db 1 MKSLDGLADTTFTTTTDLVYGSNDIQVEDIKGDWASKLGYFPQKPLTSFRGSPFQE 60

Qy 61 KMTAGDNPQLVPADQVNITEFYKSLSSFKENEENIQCGENFMDEICFVNLNPSQOLAIA 120
Db 61 KMTAGDNPQLVPADQVNITEFYKSLSSFKENEENIQCGENFMDEICFVNLNPSQOLAIA 120

Qy 121 VLSLTGLTFTVLENLVLCVILHSRSLRCRPSYHFHIGSLAVADLLGSVIFYSFIDFHFV 180
Db 121 VLSLTGLTFTVLENLVLCVILHSRSLRCRPSYHFHIGSLAVADLLGSVIFYSFIDFHFV 180

Qy 181 HRKDSRNVLFPKLGWVTASFTASVGSFLFLTAIARYISIHRLAYKRIVTRPKAVVAFCLM 240
Db 181 HRKDSRNVLFPKLGWVTASFTASVGSFLFLTAIARYISIHRLAYKRIVTRPKAVVAFCLM 240

Qy 241 WTIAIVAVLPLLGWNCCKLQSCSDIFPHIDETFLMFWIGTSLVLLFIYAYMYILWK 300
Db 241 WTIAIVAVLPLLGWNCCKLQSCSDIFPHIDETFLMFWIGTSLVLLFIYAYMYILWK 300

Db 241 WTIAIVIAVPLLGWNCCKLQSCVSDIPPHIDETVLMFWIGVTSVLLLFIVVAYMYLWK 300
|||||
Qy 301 AHSHAVRMIQRTQKSIITHTSDGKQVQVTRPDQARMAIRLAKTLVLILVLLIICWGPILL 360
|||||
Db 301 AHSHAVRMIQRTQKSIITHTSDGKQVQVTRPDQARMDIRLAKTLVLILVLLIICWGPILL 360
|||||
Qy 361 AIMVYDVFGKMKKLIKTVPFACSMCLLNSTVNPPIIYALRSKDLRHAFRSMPPSCBGTAA 420
|||||
Db 361 AIMVYDVFGKMKKLIKTVPFACSMCLLNSTVNPPIIYALRSKDLRHAFRSMPPSCBGTAA 420
|||||
Qy 421 PLDMSGDSCLHGHANNAASVHRAAESCIKSTVKIAKVTMSVSTDTSAEAL 472
|||||
Db 421 PLDMSGDSCLHGHANNAASVHRAAESCIKSTVKIAKVTMSVSTDTSAEAL 472
|||||

RESULT 10

AEA81221
ID AEA81221 standard; protein; 472 AA.

AC AEA81221;

XX 25-AUG-2005 (first entry)

DT Human cannabinoid receptor 1 (brain) variant 1 protein.

DE screening; obesity; nutritional disorder; anorectic;
KW cannabinoid receptor 1.

XX Homo sapiens.

OS US2005136465-A1.

PN 23-JUN-2005.

PD 22-DEC-2004; 2004US-00019829.

PR 22-DEC-2003; 2003EP-00104902.

XX (CLER/) CLERC R G.

PA (DUCH/) DUCHATEAU-NGUYEN G.

PA (GARD/) GARDES C.

PA (MIZR/) MIZRAHI J.

PA (OSTE/) OSTENSON C.

XX Clerc RG, Duchateau-Nguyen G, Gardes C, Mizrahi J, Ostenson C;

PI WPI; 2005-457507/46.

XX N-PSDB; AEA81160.

XX Screening test compounds that reduce and/or prevent obesity involves
XX contacting cell expressing gene from alpha-two-glycoprotein.

PS Claim 18; SEQ ID NO 88; 21pp; English.

XX The invention relates to a novel method for screening for test compounds
XX that reduce and/or prevent obesity. The method comprises contacting a
XX cell expressing a gene selected from SEQ ID NO. 1-12 or 25-85, with a
XX compound. The method of the invention demonstrates anorectic applications
XX and may be useful for screening for compounds that reduce and/or prevent
XX obesity. The current sequence is that of the human cannabinoid receptor 1
XX (brain) variant 1 protein of the invention. The sequence listing for the
XX specification can be located via the USPTO web-site.

XX Sequence 472 AA;

Query Match 99.5%; Score 2412; DB 9; Length 472;

Best Local Similarity 99.6%; Pred. No. 3.8e-240;

Matches 470; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MKSILDLADTTTTRITDLYGSDNDIQYEDIKGDMASKLGYFPQKFLTSRGSPPQE 60

Db 1 MKSILDLADTTTTRITDLYGSDNDIQYEDIKGDMASKLGYFPQKFLTSRGSPPQE 60

Qy 61 KMTAGDNPOLVPADQVNITEFYNKSLSSFKENEENIQCGENFMDIECFMVLNPSQOLAIA 120
|||||
Db 61 KMTAGDNPOLVPADQVNITEFYNKSLSSFKENEENIQCGENFMDIECFMVLNPSQOLAIA 120
|||||
Qy 121 VLSLTGLTFTVLENLILVCVILHRSRLRCRPSYHFHIGSLAVADLLGSLVFVYSFIDFHV 180
|||||
Db 121 VLSLTGLTFTVLENLILVCVILHRSRLRCRPSYHFHIGSLAVADLLGSLVFVYSFIDFHV 180
|||||
Qy 181 HRKDSRNVPFLKGGVTASFTASVGLSLFLTAARVYISHRPLAYKRIIVTRPKAVAFCLM 240
|||||
Db 181 HRKDSRNVPFLKGGVTASFTASVGLSLFLTAARVYISHRPLAYKRIIVTRPKAVAFCLM 240
|||||
Qy 241 WTIAIVIAVPLLGWNCCKLQSCVSDIPPHIDETVLMFWIGVTSVLLLFIVVAYMYLWK 300
|||||
Db 241 WTIAIVIAVPLLGWNCCKLQSCVSDIPPHIDETVLMFWIGVTSVLLLFIVVAYMYLWK 300
|||||
Qy 301 AHSHAVRMIQRTQKSIITHTSDGKQVQVTRPDQARMAIRLAKTLVLILVLLIICWGPILL 360
|||||
Db 301 AHSHAVRMIQRTQKSIITHTSDGKQVQVTRPDQARMDIRLAKTLVLILVLLIICWGPILL 360
|||||
Qy 361 AIMVYDVFGKMKKLIKTVPFACSMCLLNSTVNPPIIYALRSKDLRHAFRSMPPSCBGTAA 420
|||||
Db 361 AIMVYDVFGKMKKLIKTVPFACSMCLLNSTVNPPIIYALRSKDLRHAFRSMPPSCBGTAA 420
|||||
Qy 421 PLDMSGDSCLHGHANNAASVHRAAESCIKSTVKIAKVTMSVSTDTSAEAL 472
|||||
Db 421 PLDMSGDSCLHGHANNAASVHRAAESCIKSTVKIAKVTMSVSTDTSAEAL 472
|||||

RESULT 11

ABB56338

ID ABB56338 standard; protein; 472 AA.

XX ABB56338;

XX 18-FEB-2002 (first entry)

XX Non-endogenous human GPCR protein, SEQ ID NO: 469.

XX Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
XX constitutively activated GPCR; agonist; disease.

OS Homo sapiens.

OS Synthetic.

XX WO200177172-A2.

XX 18-OCT-2001.

XX 05-APR-2001; 2001WO-US011098.

XX 07-APR-2000; 2000US-0195747P.

XX (AREN-) ARENA PHARM INC.

XX Lehmann-Bruinsma K, Liauw CW, Lin I;

XX WPI; 2001-648759/74.

XX N-PSDB; ABI97974.

XX Identifying agonists of G protein-coupled receptors (GPCRs) for use in
XX disease treatment, comprises contacting candidate compounds with versions
XX of GPCRs.

XX Claim 1; Page 270-271; 394pp; English.

XX The invention relates to G protein-coupled receptors (GPCRs) for which
XX the endogenous ligand has been identified. Non-endogenous constitutively
XX activated versions of known GPCRs are used in the invention for the
XX direct identification of candidate compounds as receptor agonists,
XX inverse agonists or partial agonists. Such agonists are useful as
XX therapeutic agents for diseases or disorders associated with GPCRs. The

present sequence is a non-endogenous version of a known human GPCR	
Sequence 472 AA;	
Query Match	99.3%; Score 2407; DB 4; Length 472;
Best Local Similarity	99.4%; Pred. No. 1.3e-239;
Matches 469; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
1	MKSILDLGADTTT
1	MKSILDLGADTTT
61	KMTAGDNPQLVPADQVNITEFY
61	KMTAGDNPQLVPADQVNITEFY
121	VLSLTGTTFTVLE
121	VLSLTGTTFTVLE
181	HRKDSRVN
181	HRKDSRVN
241	WTIAIVIAVLP
241	WTIAIVIAVLP
301	AHSHAVRMI
301	AHSHAVRMI
361	AIMYDVF
361	AIMYDVF
421	PLNSMGDS
421	PLNSMGDS
RESULT 12	
ADN38920	
D	ADN38920 standard; protein; 472 AA.
X	ADN38920;
X	17-JUN-2004 (first entry)
T	Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:238.
X	Human; differential expression; cancer; angiogenic disorder;
X	fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
W	inflammatory disease; autoimmune disease;
W	retinal neovascularisation syndrome; scarring; uterine fibroid;
W	detection; diagnosis; prognosis; drug screening; drug targeting;
W	wound healing; contraception; cytostatic; cardiant; immunomodulatory;
W	vulnerable; gene therapy; vaccine.
S	Homo sapiens.
N	WO2003042661-A2.
N	22-MAY-2003.
D	13-NOV-2002; 2002WO-US036810.
X	13-NOV-2001; 2001US-0350666P.
R	21-NOV-2001; 2001US-0332464P.
R	29-NOV-2001; 2001US-0334393P.
R	03-DEC-2001; 2001US-0335394P.
R	14-DEC-2001; 2001US-0340376P.
R	08-JAN-2002; 2002US-0347211P.

Db 301 AHSHAVRMIOQTQKSIITHTSDGKVQVTRPDQARMDIRLAKTLVLVLIIICWGPLL 360
QY 361 AIWYDVFGKMKLIKTVPFACSMCLLNSTVNPPIIYALRSKDLRHAFRSMFPSCBGTQA 420
Db 361 AIWYDVFGKMKLIKTVPFACSMCLLNSTVNPPIIYALRSKDLRHAFRSMFPSCBGTQA 420
QY 421 PLDNSMGSDCLHKHANNAAVHRAAESCIKSTVKIAKVTMSVSTDTSAEAL 472
Db 421 PLDNSMGSDCLHKHANNAAVHRAAESCIKSTVKIAKVTMSVSTDTSAEAL 472

RESULT 13
AAR14195
ID AAR14195 standard; protein; 473 AA.
XX AAR14195;
XX AC
XX 25-MAR-2003 (revised)
DT 17-DEC-2001 (revised)
DT 19-DEC-1991 (first entry)
XX
XX Rat cannabinoid receptor SKR6.
XX Cannabis sativa; marijuana; drug test; substance K receptor.
XX Rattus.
XX
XX Key Location/Qualifiers
FT Modified-site 78
FT /label= OTHER
FT /note= "N-glycosylated"
FT Modified-site 84
FT /label= OTHER
FT /note= "N-glycosylated"
FT Modified-site 113
FT /label= OTHER
FT /note= "N-glycosylated"
FT Domain 118..143
FT /label= hydrophobic_domain_I
FT Domain 156..173
FT /label= hydrophobic_domain_II
FT Domain 189..213
FT /label= hydrophobic_domain_III
FT Domain 234..256
FT /label= hydrophobic_domain_IV
FT Domain 276..300
FT /label= hydrophobic_domain_V
FT Domain 346..366
FT /label= hydrophobic_domain_VI
FT Domain 379..400
FT /label= hydrophobic_domain_VII
XX USN7564075-N.
XX
XX 03-SEP-1991.
XX
XX 08-AUG-1990; 90US-00564075.
XX
XX 08-AUG-1990; 90US-00564075.
XX
XX (USSH) NAT INST OF HEALTH.
PA (USDC) US SEC OF COMMERCE.
XX
XX Matsuda L, Brownstein M;
XX WPI; 1991-303326/41.
XX
XX DNA encoding mammalian cannabinoid receptor - used for producing receptor
PT for screening drugs and ligands and in detection.
XX
XX Disclosure; Fig 1; 25pp; English.
XX
XX SKR6 cDNA encoding the rat cannabinoid receptor was isolated from a rat

CC cerebral cortex cDNA library. An EcoRI-XbaI fragment was used to screen a
CC human cosmid library and a positive clone was identified. There is ca. 97
CC per cent homology between the deduced amino acid sequences of the human
CC and rat cannabinoid receptors. The specification includes the sequence of
CC a cDNA fragment which encodes this rat cannabinoid receptor protein but
CC the copy quality is extremely poor. Recombinantly produced receptor can
CC be used to screen for new drugs suitable for treatment of cannabinoid-
CC treatable conditions, e.g. glaucoma, bronchial asthma, etc. See AAR14003
CC and AAR14196 for human cannabinoid receptor sequences. (Note: Revised
CC entry submitted to correct the patent number format of US Government-
CC owned NTIS applications to prevent clashes with ongoing US granted patent
CC numbers. For further information please visit the Derwent web site at
CC www.derwent.com/dwpi/updates/ntis_us.html.) (Updated on 25-MAR-2003 to
CC correct PA field.)
XX
XX SQ Sequence 473 AA;
Query Match 96.7%; Score 2343.5; DB 2; Length 473;
Best Local Similarity 96.8%; Pred. No. 4.7e-233;
Matches 458; Conservative 5; Mismatches 9; Indels 1; Gaps 1;
QY 1 MKSILDGLADTTFRITITDLYVGSNDIOYEDIKGMASKLGYFPQKPLTSFRGSPFOE 60
Db 1 MKSILDGLADTTFRITITDLYVGSNDIOYEDIKGMASKLGYFPQKPLTSFRGSPFOE 60
QY 61 KMTAGDNPOLVPA-DQVNIETFYFNKLSFSFKENEENIQCGENFMDECFMILNPSQOLAI 119
Db 61 KMTAGDNPOLVPA-DQVNIETFYFNKLSFSFKENEENIQCGENFMDECFMILNPSQOLAI 120
QY 120 AVLSTLTGFTVLENLVLCVILHSRLRCRPSYHFIGSLAVADLLGSIFFVYSFIDFHV 179
Db 121 AVLSTLTGFTVLENLVLCVILHSRLRCRPSYHFIGSLAVADLLGSIFFVYSFIDFHV 180
QY 180 FHRKDSRVFLFKIGVTSFTASVGSFLTAIARYISIHRLAYKRIIVTRPKAVVAFCL 239
Db 181 FHRKDSRVFLFKIGVTSFTASVGSFLTAIARYISIHRLAYKRIIVTRPKAVVAFCL 240
QY 240 MWTIAIVIAVLELLGNCKEQLQSCVDIPPHIDETVLMFVIGVTSVLLFIIVAYMYILW 299
Db 241 MWTIAIVIAVLELLGNCKEQLQSCVDIPPHIDETVLMFVIGVTSVLLFIIVAYMYILW 300
QY 300 KAHSHAVRMIOQTQKSIITHTSDGKVQVTRPDQARMAIRLAKTLVLVLIIICWGPL 359
Db 301 KAHSHAVRMIOQTQKSIITHTSDGKVQVTRPDQARMAIRLAKTLVLVLIIICWGPL 360
QY 360 LAIMYDVFGKMKLIKTVPFACSMCLLNSTVNPPIIYALRSKDLRHAFRSMFPSCBGT 419
Db 361 LAIMYDVFGKMKLIKTVPFACSMCLLNSTVNPPIIYALRSKDLRHAFRSMFPSCBGT 420
QY 420 QPLDNSMGSDCLHKHANNAAVHRAAESCIKSTVKIAKVTMSVSTDTSAEAL 472
Db 421 QPLDNSMGSDCLHKHANNAAVHRAAESCIKSTVKIAKVTMSVSTDTSAEAL 473

RESULT 14
ADD46381
ID ADD46381 standard; protein; 473 AA.
XX
XX AC ADD46381;
XX
XX 29-JAN-2004 (first entry)
XX
XX Rat Protein P20272, SEQ ID NO 12061.
XX
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX Chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
XX Rattus norvegicus.
XX
XX WO2003016475-A2.
XX
XX 27-FEB-2003.
XX

PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
PA
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
XX GENBANK; P20272.
DR
DR
XX
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
PT
XX
XX
XX Claim 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX
XX Sequence 473 AA;

Query Match 96.7%; Score 2343.5; DB 7; Length 473;
Best Local Similarity 96.8%; Pred. No. 4.7e-233;
Matches 458; Conservative 5; Mismatches 9; Indels 1; Gaps 1;
QY 1 MKSILDGLADTTFTTTTDLVGSNDIQYEDIKGDMASKLGYFPQKPLTSFRGSPQE 60
DB 1 MKSILDGLADTTFTTTTDLVGSNDIQYEDIKGDMASKLGYFPQKPLTSFRGSPQE 60
QY 61 KMTAGDNPQLVPA-DQVNITEFYNKSLSGSPKNEBENIQCGENFMDIECFMVLNPSQQLAI 119
DB 61 KMTAGDNPQLVPA-DQVNITEFYNKSLSGSPKNEBENIQCGENFMDIECFMVLNPSQQLAI 120
QY 120 AVLSLTGTFTVLENLLVLCVILHSRSLRCPSPHYFISGLAVADLLGSIIVFVSPIDPHV 179
DB 121 AVLSLTGTFTVLENLLVLCVILHSRSLRCPSPHYFISGLAVADLLGSIIVFVSPIDPHV 180
QY 180 FHRKDSRNVLFLKGGVTASTASVGSFLTAIRYISIHRLPAYKRVITRPKAVAFCL 239
DB 181 FHRKDSRNVLFLKGGVTASTASVGSFLTAIRYISIHRLPAYKRVITRPKAVAFCL 240
QY 240 MWTIAIVAVLPFLGWNCKQLQSVCSDFIPPHIDETYLMTFVIGVTSVLLLFIVAYMYILW 299
DB 241 MWTIAIVAVLPFLGWNCKQLQSVCSDFIPPHIDETYLMTFVIGVTSVLLLFIVAYMYILW 300

QY 300 KAHSHAVRMIOQGTOKSIIHTSDEGKVQVTRPDQARMALRLAKTLVLILVLIICWGPL 359
DB 301 KAHSHAVRMIOQGTOKSIIHTSDEGKVQVTRPDQARMALRLAKTLVLILVLIICWGPL 360
QY 360 LAIMVYDVFGKNNKLIKTVFAPCSMLCLANSTVNPPIIYALRSKDLRHAFSPSCSGTA 419
DB 361 LAIMVYDVFGKNNKLIKTVFAPCSMLCLANSTVNPPIIYALRSKDLRHAFSPSCSGTA 420
QY 420 QPLDNSMGSDCLLKHANNAASVHRAAESCIKSTVKIAKVTMSVSTDTSAEAL 472
DB 421 QPLDNSMGSDCLLKHANNTASMHRAAESCIKSTVKIAKVTMSVSTDTSAEAL 473
RESULT 15
ABB57048
ID ABB57048 standard; protein; 473 AA.
XX ABB57048;
XX 07-MAR-2002 (first entry)
DT Mouse ischaemic condition related protein sequence SEQ ID NO:77.
DE Mouse ischaemic condition related protein sequence SEQ ID NO:77.
XX Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
KW vasospastic ischaemia; ischaemic condition; ischaemic disease.
XX Mus musculus.
XX WO200188188-A2.
XX 22-NOV-2001.
XX 18-MAY-2001; 2001WO-JP004192.
XX 18-MAY-2000; 2000JP-00145977.
XX (UYN1-) UNIV NIHON SCHOOL JURIDICAL PERSON.
XX Ishikawa K, Aesai S, Takahashi Y, Nagata T, Ishii Y;
XX WPI; 2002-034733/04.
DR N-PSDB; ABI99249.
XX
XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring
PT expression levels of particular genes defined in the specification or by
PT determining the expression profile of a gene group comprising these
PT genes.
XX
XX Claim 2; Page 235-237; 2690pp; English.
XX
XX The present invention describes a method for examining ischaemic
CC conditions, comprising measuring the expression levels of particular
CC genes (I) in a test sample or determining the expression profile of a
CC gene group in the sample comprising genes selected from (I). The method
CC is useful for examining the ischaemic condition (e.g. compressive
CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
CC expression levels of particular genes (ABI99202 to ABI99912, encoding the
CC protein sequences in ABB57020 to ABB57374) or by determining the
CC expression profile of a gene group comprising these genes. The expression
CC levels or expression profiles produced by these genes are used as an
CC indicator when screening for ischaemic condition-improving drugs or
CC therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR
CC primers for a mouse ischaemic condition related sequence, which are used
CC in the exemplification of the present invention
XX
XX Sequence 473 AA;
Query Match 96.6%; Score 2340.5; DB 5; Length 473;
Best Local Similarity 96.6%; Pred. No. 9.6e-233;
Matches 457; Conservative 6; Mismatches 9; Indels 1; Gaps 1;
QY 1 MKSILDGLADTTFTTTTDLVGSNDIQYEDIKGDMASKLGYFPQKPLTSFRGSPQE 60
|||||

Db 1 MKSILDGLADTTFRITTTDLVYVGSNDIQYEDIKGDMSKLGYPQKFPFLTFRGSPFOE 60
Qy 61 KMTAGNPOLVPA-DQVNITEFYNKSLSSFKENEENIQCGENFMDIECFMVLNPSOQLAI 119
Db 61 KMTAGNSPLVPAGDTNITEFYNKSLSSFKENEDNIQCGENFMDMECFMVLNPSOQLAI 120
Qy 120 AVLSLTGTFVLENLVLCVILHRSRLRCRPSYHFIGSLAVADLLGSI FVYSFIDPHV 179
Db 121 AVLSLTGTFVLENLVLCVILHRSRLRCRPSYHFIGSLAVADLLGSI FVYSFVDFHV 180
Qy 180 FHRKDSRNVLFLKGGVTASFTASVGSFLTAIARIYISHRPLAYKRIVTRPKAVVAFCL 239
Db 181 FHRKDSPNVFLKGGVTASFTASVGSFLTAIDRYISHRPLAYKRIVTRPKAVVAFCL 240
Qy 240 MMTIAIVIAVLPLLGWNCCKLOSVCSDIPPHIDETVLMFWIGVTSVLLLFIVYAYMILM 299
Db 241 MMTIAIVIAVLPLLGWNCCKLOSVCSDIPFLIDETVLMFWIGVTSVLLLFIVYAYMILM 300
Qy 300 KAHSHAVRMIQRTQKSIITHTSEDKGVQVTRPDQARMAIRLAKTLVLVLVLIICWGEL 359
Db 301 KAHSHAVRMIQRTQKSIITHTSEDKGVQVTRPDQARMDIRLAKTLVLVLVLIICWGEL 360
Qy 360 LAIMVYDVFQKXNKLIKTVPFCSMLCLLNSTVNPITIALRSKDLRHAFRSMFPSCGTA 419
Db 361 LAIMVYDVFQKXNKLIKTVPFCSMLCLLNSTVNPITIALRSKDLRHAFRSMFPSCGTA 420
Qy 420 OPLDMSMGSDCLHKHANNAAVHRAESCIKSTVKIATVMTSVSTDTSAEAL 472
Db 421 OPLDMSMGSDCLHKHANNATSMHRAESCIKSTVKIATVMTSVSTDTSAEAL 473

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OM protein - protein search, using sw model

Run on: January 6, 2006, 21:08:38 ; Search time 13 Seconds

(without alignments)
308.138 Million cell updates/sec

Title: US-10-521-420-1

Perfect score: 2424

Sequence: 1 MKSLDGLADTTFTTTDL.....TVKIAKVTMSVSDTSAEAL 472

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 61072 seqs, 8486849 residues

Total number of hits satisfying chosen parameters: 61072

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /cgn2_5/ptodata/2/pubpa/US08_NEW_PUB_PEP.*
- 2: /cgn2_6/ptodata/2/pubpa/US06_NEW_PUB_PEP.*
- 3: /cgn2_6/ptodata/2/pubpa/US07_NEW_PUB_PEP.*
- 4: /cgn2_6/ptodata/2/pubpa/US09_NEW_PUB_PEP.*
- 5: /cgn2_6/ptodata/2/pubpa/US10_NEW_PUB_PEP.*
- 6: /cgn2_6/ptodata/2/pubpa/US11_NEW_PUB_PEP.*
- 7: /cgn2_6/ptodata/2/pubpa/US60_NEW_PUB_PEP.*
- 8: /cgn2_6/ptodata/2/pubpa/US60_NEW_PUB_PEP.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2412	99.5	472	7	US-11-127-877-39
2	710	29.3	360	6	US-10-851-667A-26
3	363	15.0	364	7	US-11-067-884-2
4	352.5	14.5	378	6	US-10-995-561-891
5	351.5	14.5	382	7	US-11-124-368A-173
6	351.5	14.5	382	7	US-11-124-368A-174
7	351.5	14.5	382	7	US-11-127-877-58
8	341	14.1	353	7	US-11-067-884-6
9	311.5	12.9	351	7	US-11-067-884-4
10	310.5	12.8	334	7	US-11-110-274-6
11	289	11.9	330	7	US-11-110-274-4
12	283	11.7	429	7	US-11-127-877-51
13	283	11.7	466	7	US-11-127-877-50
14	280	11.6	362	7	US-11-110-274-5
15	272	11.2	360	6	US-10-995-561-547
16	248.5	10.3	254	6	US-10-055-877-248
17	248.5	10.3	254	6	US-10-055-877-327
18	248.5	10.3	254	6	US-10-055-877-340
19	235.5	9.7	797	6	US-10-995-561-802
20	231.5	9.6	317	6	US-10-995-561-798
21	228	9.4	318	7	US-11-127-877-38
22	222.5	9.2	480	6	US-10-521-162-40
23	221	9.1	259	6	US-10-055-877-225
24	221	9.1	259	6	US-10-055-877-237
25	216.5	8.9	471	6	US-10-995-561-901

26	213	8.8	365	6	US-10-875-716-9	Sequence 9, Appli
27	209	8.6	384	7	US-11-080-991-26	Sequence 26, Appli
28	201	8.3	412	7	US-11-170-153-8	Sequence 8, Appli
29	201	8.3	412	7	US-11-170-166-8	Sequence 8, Appli
30	201	8.3	412	7	US-11-170-351-8	Sequence 8, Appli
31	201	8.3	415	7	US-11-170-153-6	Sequence 6, Appli
32	201	8.3	415	7	US-11-170-166-6	Sequence 6, Appli
33	201	8.3	415	7	US-11-170-351-6	Sequence 56, Appli
34	198	8.2	407	7	US-11-127-877-56	Sequence 4, Appli
35	197	8.1	412	7	US-11-170-153-4	Sequence 4, Appli
36	197	8.1	412	7	US-11-170-166-4	Sequence 4, Appli
37	197	8.1	412	7	US-11-170-351-4	Sequence 2, Appli
38	197	8.1	415	7	US-11-170-153-2	Sequence 2, Appli
39	197	8.1	415	7	US-11-170-166-2	Sequence 2, Appli
40	197	8.1	415	7	US-11-170-351-2	Sequence 55, Appli
41	195	8.0	400	7	US-11-127-877-55	Sequence 45, Appli
42	195	8.0	415	7	US-11-127-877-45	Sequence 157, App
43	194.5	8.0	757	6	US-10-055-877-157	Sequence 12, Appli
44	194	8.0	712	6	US-10-521-162-12	Sequence 160, App
45	193	8.0	1115	6	US-10-055-877-160	

ALIGNMENTS

RESULT 1

US-11-127-877-39
; Sequence 39, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 39
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-127-877-39

Query Match	99.5%	Score 2412;	DB 7;	Length 472;
Best Local Similarity	99.6%	Pred. No. 6e-199;		
Matches	470;	Conservative	0;	Mismatches 2;
Indels	0;	Gaps	0;	
Qy	1	MKSILDLGLADTTFTTTTDLVGSNDIQVEDIKGDWASKLGYFPQKPLTSFRGSPQOE	60	
Db	1	MKSILDLGLADTTFTTTTDLVGSNDIQVEDIKGDWASKLGYFPQKPLTSFRGSPQOE	60	
Qy	61	KMTAGDNPQLVPADQVNITEFYKSLSSFKENEENIQCGENFMDEICFVNLNPSQOLAIA	120	
Db	61	KMTAGDNPQLVPADQVNITEFYKSLSSFKENEENIQCGENFMDEICFVNLNPSQOLAIA	120	
Qy	121	VLSLTGLTFTVLENLVLCVILHRSRSCRSYHFIGSLAVADLLGSLVIVYSFTDFHVF	180	
Db	121	VLSLTGLTFTVLENLVLCVILHRSRSCRSYHFIGSLAVADLLGSLVIVYSFTDFHVF	180	
Qy	181	HRKDSRVFLPKLGVGTASTASVGSLSFLTAIARYISIHRLAYKRIIVTRPKAVVAFCLM	240	
Db	181	HRKDSRVFLPKLGVGTASTASVGSLSFLTAIARYISIHRLAYKRIIVTRPKAVVAFCLM	240	
Qy	241	WTIAIVIAVLELLGNCKLQSCVDIPPHIDEVYLMFWIGVTSVLLLFIVTAYNYILWK	300	
Db	241	WTIAIVIAVLELLGNCKLQSCVDIPPHIDEVYLMFWIGVTSVLLLFIVTAYNYILWK	300	

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Db 241 WTIAIVAVLPLGMNCEKLSQVCSDFPHIDETVLMFVIGVTSVLLLFIVVAYMYLWK 300
Qy 301 AHSHAVRMIOQTGKSIHHTSDGKVQVTRPDQARMAIRLAKTLVLVLIIICWGPILL 360
Db 301 AHSHAVRMIOQTGKSIHHTSDGKVQVTRPDQARMDIRLAKTLVLVLIIICWGPILL 360
Qy 361 AIMVDVFGKMKLIKTVFAFCMLCLLNSTVNPPIIYALRSKDLRHAFRSMFPSCBGTQA 420
Db 361 AIMVDVFGKMKLIKTVFAFCMLCLLNSTVNPPIIYALRSKDLRHAFRSMFPSCBGTQA 420
Qy 421 PLDNSMGDSCLHKHANNAAVHRAAESCIKSTVKIAKVTMSVSTDTSAEAL 472
Db 421 PLDNSMGDSCLHKHANNAAVHRAAESCIKSTVKIAKVTMSVSTDTSAEAL 472

RESULT 2
US-10-851-667A-26
; Sequence 26, Application US/10851667A
; Publication No. US20050260608A1
; GENERAL INFORMATION:
; APPLICANT: Zimmer, Andreas
; APPLICANT: Karsak, Meliha
; APPLICANT: de Vernejoul, Marie-Christine
; APPLICANT: Bab, Itai
; APPLICANT: Shohami, Esther
; APPLICANT: Mechoulam, Raphael
; TITLE OF INVENTION: DELAYING ONSET OF, PREVENTING AND/OR TREATING OSTEOPOROSIS
; FILE REFERENCE: 28030
; CURRENT APPLICATION NUMBER: US/10/851,667A
; CURRENT FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (63)-(63)
; OTHER INFORMATION: Non-synonymous polymorphism: Gln or Arg
US-10-851-667A-26

Query Match 29.3%; Score 710; DB 6; Length 360;
Best Local Similarity 45.2%; Pred. No. 1.2e-53;
Matches 149; Conservative 57; Mismatches 94; Indels 30; Gaps 6;

Qy 78 ITFYNKSLSSFKENEENIQCGENFMDIECFMVLNPSQQLAIAVLSLTGFTVLENLIV 137
Db 6 VTEIANGSKDGLDSN-----PMKDYMLISGPQKTAVALCTLLGLLSALENAV 54
Qy 138 LCVILHSRLRCPSPSYHFTGSLAVADLLGSLVIFVYFIDFPHFRKDSRNVLFLKLGVT 197
Db 55 LYLISSHLLRKPSPVLFITGSLAGADFLASWFACSFVNFPHVGHVDSKAVFLKLGVT 114
Qy 198 ASPTASVGSFLTAIARYISIHRLAYKRVTRPKAVAFCLMWTIAIVAVLPLLGWNC 257
Db 115 MPTASVGSLLTAIDRYLCRLYPSPYKALLIFGRALVTLGIMVLSALVSLPLMGWTC 174
Qy 258 EKLQSVCSDFPHIDETVLMFVIGVTSVLLLFIVVAYMYLWKASHAVRMIOQTGKSI 317
Db 175 --CPRCESELFPIPNLYLLSWLLFTAFIFSGIITYGHVLMKHAQHVA-----SL 223
Qy 318 IHTSDGKVQVTRPDQARMA--IRLAKTLVLVLIIICWGPILLAIMVDVFGKMKLIK 375
Db 224 SGH--QDRQV----PGKARMLRDRLAKTLGLVLAVLLICWFPVLALMAHSATLISDQV 277
Qy 376 KTVFAFCMLCLLNSTVNPPIIYALRSKDLR 405
Db 278 KKAFAFCMLCLLNSTVNPPIIYALRSGEIR 307

RESULT 3
```

```
US-11-067-884-2
; Sequence 2, Application US/11067884
; Publication No. US20050261252A1
; GENERAL INFORMATION:
; APPLICANT: Miller, Duane D.
; APPLICANT: Tigyi, Gabor
; APPLICANT: Dalton, James T.
; APPLICANT: Sardar, Vineet M.
; APPLICANT: Elrod, Don B.
; APPLICANT: Xu, Huiping
; APPLICANT: Baker, Daniel L.
; APPLICANT: Wang, Dean
; APPLICANT: Lillom, Karoly
; APPLICANT: Fischer, David J.
; APPLICANT: Virag, Tamas
; APPLICANT: Nusser, Nora
; TITLE OF INVENTION: LPA RECEPTOR AGONISTS AND ANTAGONISTS AND METHODS OF
; TITLE OF INVENTION: USE
; FILE REFERENCE: 20609/305
; CURRENT APPLICATION NUMBER: US/11/067,884
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 60/190,370
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 09/811,838
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-067-884-2

Query Match 15.0%; Score 363; DB 7; Length 364;
Best Local Similarity 27.2%; Pred. No. 5.5e-24;
Matches 108; Conservative 72; Mismatches 167; Indels 50; Gaps 10;

Qy 59 QEKMTAGNPQLPVADQVNIETEFYKNSLSSPKENEENIQCGENFMDIECFMVLNPSQQLA 118
Db 13 QPQFTAMNEPQC-----FYNESIAFFYNNRSGKHLATE-----WNTVSKLV 52
Qy 119 IAVLSLTGFTVLENLIVLCVILHSRLRCPSPSYHFTGSLAVADLLGSLVIFVYFIDFH 178
Db 53 MG-LGITVCIFITMLANLLVMVAIVYNNRRFHP-FIYLLMANLAAADFFAGLAYFYLMNTG 110
Qy 179 VFHRKDSRNVLFLKLGVTASTASVGSFLTAIARYISIHRLAYKRVTRPKAVAFVC 238
Db 111 PNTRRLITVSTWLLRQGLIDTSLTASVANLLATAIERHITVFRMQLHTRMSNR-RVVVVIV 169
Qy 239 LMWTIAIVAVLPLLGWNCCKLQSVCSDFPHIDETVLMFVIGVTSVLLLFIVVAYMYL 298
Db 170 VIWTVAIVMGAIPSGWNCICDIENCSNMAPLYSDSLVFVAIFNLVTFVWVWVLYAHIF 229
Qy 299 WKAHSHAVRMIOQTGKSIHHTSDGKVQVTRPDQARMAIRLAKTLVLVLIIICWGP 358
Db 230 GYVORTMMSR-----HSSGPRNRD-----MMSLLKTVVIVLGAFFIICWTP 273
Qy 359 LLAIWVYDVFGKMKLIKTVFAFCMLCLLNSTVNPPIIYALRSKDLRHAFRSMFPSCBGT 418
Db 274 GLVLLLDVCCQCQDVL-AYEKFFLLLAEFNANMNPPIIYSDRKEMSAIFRQIL-----C 327
Qy 419 AQLDNSMGDSCLHKHANN-----AASVHRAAESCI 450
Db 328 QRSENPQTGPTSSDRSASSLNHTILAGVHSDHVSU 364

RESULT 4
US-10-995-561-891
; Sequence 891, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
```

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; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 891
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-891

Query Match 14.5%; Score 352.5; DB 6; Length 378;
Best Local Similarity 29.7%; Pred. No. 4.6e-23;
Matches 105; Conservative 61; Mismatches 131; Indels 57; Gaps 13;

QY 121 VLSLTGTFVLENLVLCVILHSRLCRPSYHFHFGSLAVADLLGVSIFVDFHVF 180
DB 44 VLFVICSFVLENLVLCVILHSRLCRPSYHFHFGSLAVADLLGVSIFVDFHVF 99
QY 181 HRKD---SRNVFLFKGGVTASFTASVGSFLFATAIARYIS---HRPL-AKRVITRPKAV 234
DB 100 GKTFSLSPVWFLREGSMFVALGASTCSLLAIAIERHLTWIKMRPYDANKR--HRVFL 157
QY 235 VAFCLMTIAIVTLVLCVILHSRLCRPSYHFHFGSLAVADLLGVSIFVDFHVF 292
DB 158 IGMG--WLIATFLGALPILGNCVILHSRLCRPSYHFHFGSLAVADLLGVSIFVDFHVF 215
QY 293 AYVILWKAHSHAVRMIRGQTKSIITHTSDGKQVQVTRPDQARMAIRLAKTLVILVWL 352
DB 216 ARIYFLVKSSR-----KVANHNSERSMALLRTVIVVSVF 252
QY 353 IICWGPLLAIMVYDFGKMK--LITVFAPCSMLCLLNSTVNPITIALRSKDLRAHFR 409
DB 253 IACWSPLFILDLVACRVQACPIKFAQWFI--VLAVLSANMPVITVTLASKEMRRAFF 310
QY 410 SMPFSC-----EGTAQPLDSMGSDCLHKHANNAAS-----VHRAAESCI 450
DB 311 RLVCNCLVRGRGARASPIQALDPSRKSSSNSHSPKVKEDLPHTAPSSCI 364

RESULT 5
US-11-124-368A-173
; Sequence 173, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: James J. Devlin
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001524
; CURRENT APPLICATION NUMBER: US/11/124,368A
; CURRENT FILING DATE: 2005-05-09
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/568,845
; PRIOR FILING DATE: 2004-11-09
; NUMBER OF SEQ ID NOS: 21112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 173
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-368A-173

Query Match 14.5%; Score 351.5; DB 7; Length 382;
Best Local Similarity 27.6%; Pred. No. 5.7e-23;
Matches 105; Conservative 67; Mismatches 125; Indels 83; Gaps 13;

QY 68 POLVP-----ADQVN---ITEFYN-----KSLSSPKENEENIQCGENFMDIECFMVL 111
DB 3 PTVPLVKAHRSVSDVYVYDIIVRHYNTGKLNISADKENSIKL----- 47
QY 112 NPSQQLAIAVLSLTGTFVLENLVLCVILHSRLCRPSYHFHFGSLAVADLLGVSIFV 171
DB 48 -----TSVVFLICCFIILENIFVLLTIWTKKFF-RPMYFIGNLALSLLAGVAYT 99
QY 172 YSFIDFVHFKDSRNVLFLKGGVTASFTASVGSFLFATAIARYIS-----IHRPLAYKR 226
DB 100 ANLLSGATTYKLTTPAQWFLREGSMFVALSASVFSLLAIAIERYITMLKMKLHNSNFR 159
QY 227 IVTRPKAVVACLMWTIAIVTLVLCVILHSRLCRPSYHFHFGSLAVADLLGVSIFV 286
DB 160 LF-----LLISAC--WVLSLILGGPIMGWNCISALSSCSVTLPLVHKHYILFCTVTFTLL 213
QY 287 LLFTV--YAYVILWKAHSHA-----VRMIQRGQTKSIITHTSDGKQVQVTRPDQARMA 338
DB 311 YTLTNKEMRRAFIRIMSCCK 330

RESULT 6
US-11-124-368A-174
; Sequence 174, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: James J. Devlin
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001524
; CURRENT APPLICATION NUMBER: US/11/124,368A
; CURRENT FILING DATE: 2005-05-09
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/568,845
; PRIOR FILING DATE: 2004-11-09
; NUMBER OF SEQ ID NOS: 21112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 174
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-368A-174

Query Match 14.5%; Score 351.5; DB 7; Length 382;
Best Local Similarity 27.6%; Pred. No. 5.7e-23;
Matches 105; Conservative 67; Mismatches 125; Indels 83; Gaps 13;

QY 68 POLVP-----ADQVN---ITEFYN-----KSLSSPKENEENIQCGENFMDIECFMVL 111
DB 3 PTVPLVKAHRSVSDVYVYDIIVRHYNTGKLNISADKENSIKL----- 47
QY 112 NPSQQLAIAVLSLTGTFVLENLVLCVILHSRLCRPSYHFHFGSLAVADLLGVSIFV 171
DB 48 -----TSVVFLICCFIILENIFVLLTIWTKKFF-RPMYFIGNLALSLLAGVAYT 99
QY 172 YSFIDFVHFKDSRNVLFLKGGVTASFTASVGSFLFATAIARYIS-----IHRPLAYKR 226
DB 100 ANLLSGATTYKLTTPAQWFLREGSMFVALSASVFSLLAIAIERYITMLKMKLHNSNFR 159
QY 227 IVTRPKAVVACLMWTIAIVTLVLCVILHSRLCRPSYHFHFGSLAVADLLGVSIFV 286
DB 160 LF-----LLISAC--WVLSLILGGPIMGWNCISALSSCSVTLPLVHKHYILFCTVTFTLL 213
QY 287 LLFTV--YAYVILWKAHSHA-----VRMIQRGQTKSIITHTSDGKQVQVTRPDQARMA 338
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Db 214 LLSIVLYCRIYSLVTRSRRLTRFRKNISKASRSSEKS----- 251
QY 339 IRLAKTLVLVLIIICWGPLLAIMVYDVGKNNKLIKTVF--AFCSMLCLLNSTVNPPII 396
Db 252 LALKTKVIVLSVFIACWAPLFLILLDDVGCKV-KTCDILFRAEYFLVLAVLNSGTNPPII 310
QY 397 YALRSKDLRHAFRSMPPSC 416
Db 311 YTLTNKEMRAFRINSCCK 330

RESULT 7
US-11-127-877-58
; Sequence 58, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 58
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-127-877-58

Query Match 14.5%; Score 351.5; DB 7; Length 382;
Best Local Similarity 27.6%; Pred. No. 5.7e-23;
Matches 105; Conservative 67; Mismatches 125; Indels 83; Gaps 13;

QY 68 PQIUP-----ADQVN---ITBFYN-----KSLSSFKEENEIOCGENFMDIECFMVL 111
Db 3 PTVPLVKAHRSSVSDVNVYDIIVRHVYVTKLNISADKENSIKL----- 47
QY 112 NPSQQLAIAVLSLTGLTFTVLENLVLCVILHSRLCRPSYHFIGSLAVADLLGSVIFV 171
Db 48 -----TSVVFILICCFIENIFVLLTIWTKKXF-RPMYYFIGNLALSDLLAGVAYT 99
QY 172 YSPIDFVHRKDSRVNLFKLGVTASTASVGSFLTAIARYIS-----IHRPLAYKR 226
Db 100 ANLLSGATTYKLTPAQWREGSMFVALSVFSLTAIAERYITMLKMKLHGNSNFR 159
QY 227 IVTRPRKAVAFCLMWTIAIVLPLLGWNCCKLQSVCSDFIPHIDETVLMFVIWTSVL 286
Db 160 LF-----LLISAC--WISLILGGLPIMGWNCISALSSCSVLPYXKHVILFCTTVFTLL 213
QY 287 LLFIV--YAYMYILWKAHSHA-----VRMIQRTQKSIHHTSBDGKVQVTRPDQARMA 338
Db 214 LLSIVLYCRIYSLVTRSRRLTRFRKNISKASRSSEKS----- 251
QY 339 IRLAKTLVLVLIIICWGPLLAIMVYDVGKNNKLIKTVF--AFCSMLCLLNSTVNPPII 396
Db 252 LALKTKVIVLSVFIACWAPLFLILLDDVGCKV-KTCDILFRAEYFLVLAVLNSGTNPPII 310
QY 397 YALRSKDLRHAFRSMPPSC 416
Db 311 YTLTNKEMRAFRINSCCK 330

RESULT 8
US-11-067-884-6
```

```
; Sequence 6, Application US/11067884
; Publication No. US20050261252A1
; GENERAL INFORMATION:
; APPLICANT: Miller, Duane D.
; APPLICANT: Tigyi, Gabor
; APPLICANT: Dalton, James T.
; APPLICANT: Sardar, Vineet M.
; APPLICANT: Elrod, Don B.
; APPLICANT: Xu, Huiping
; APPLICANT: Baker, Daniel L.
; APPLICANT: Wang, Dean
; APPLICANT: Lillem, Karoly
; APPLICANT: Fischer, David J.
; APPLICANT: Nusser, Nora
; TITLE OF INVENTION: LPA RECEPTOR AGONISTS AND ANTAGONISTS AND METHODS OF
; TITLE OF INVENTION: USE
; FILE REFERENCE: 20609/305
; CURRENT APPLICATION NUMBER: US/11/067,884
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 60/190,370
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 09/811,838
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-067-884-6

Query Match 14.1%; Score 341; DB 7; Length 353;
Best Local Similarity 26.9%; Pred. No. 4e-22;
Matches 80; Conservative 68; Mismatches 123; Indels 26; Gaps 6;

QY 121 VLSLTGLTFTVL-----ENLLVLCVILHSRLCRPSYHFIGSLAVADLLGSVIFVYSFD 176
Db 31 VIVLCVGTFFCLFIPFNSLVIAAVIKNRKHF-PFYLLANLAADFFAGIAYVFLMFN 89
QY 177 FHVFRKDSRVNLFKLGVTASTASVGSFLTAIARYIS-IHRPLAYKRIVTRPKAVVA 236
Db 90 TGPVSKTLTNVNFURQGLDSSLTASLTNLIIVAVERHMSIMRMRVHNSL-TKKRVTL 148
QY 237 FCLMTIATIAIVLPLLGWNCCKLQSVCSDFIPHIDETVLMFVI--GVTSVLLFLFVYAY 294
Db 149 ILLVMAIAIFMGAVPTLGWNCCLNCSACSLAPIYSRSLVFWTVSNLMAFLIMVVYL 208
QY 295 MYLWKAHSHAVRMIOQTQKSIHHTSBDGKVQVTRPDQARMAIRLAKTLVLVLII 354
Db 209 IVVYVK-----RKTNVLSPHTSGSI-----SRRRTPMKLMKMTVMTVLGAFV 250
QY 355 CWGPLLAIMVYDVGKNNKLIKTVFACSMCLLNSTVNPPIIYALRSKDLRHAFRSM 411
Db 251 CWTPLGLVLLDGLNCRQCGVQHVKRWFLLALLNSVNPPIIYSYKDEDMYGTMKKM 307

RESULT 9
US-11-067-884-4
; Sequence 4, Application US/11067884
; Publication No. US20050261252A1
; GENERAL INFORMATION:
; APPLICANT: Miller, Duane D.
; APPLICANT: Tigyi, Gabor
; APPLICANT: Dalton, James T.
; APPLICANT: Sardar, Vineet M.
; APPLICANT: Elrod, Don B.
; APPLICANT: Xu, Huiping
; APPLICANT: Baker, Daniel L.
; APPLICANT: Wang, Dean
; APPLICANT: Lillem, Karoly
; APPLICANT: Fischer, David J.
; APPLICANT: Virag, Tamas
```



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; APPLICANT: Nusser, Nora
; TITLE OF INVENTION: LPA RECEPTOR AGONISTS AND ANTAGONISTS AND METHODS OF
; TITLE OF INVENTION: USE
; FILE REFERENCE: 20609/305
; CURRENT APPLICATION NUMBER: US/11/067,884
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 60/190,370
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 09/811,838
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 4
; LENGTH: 351
; TYPE: PR1
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-11-067-884-4

Query Match 12.9%; Score 311.5; DB 7; Length 351;
Best Local Similarity 27.0%; Pred. No. 1.3e-19;
Matches 90; Conservative 60; Mismatches 150; Indels 33; Gaps 10;

QY 81 FYNKLSFKEBENIQCFMDFMVLNPSQQLAIAVLSLTGFTVLENLVLGV 140
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 8 YNETIGFFYNSGK-----ELSHWRPKDQVVVA-LGLTVSLVLLTNLAVIA 56

QY 141 ILHSRLRCPSTHPTGSLAVADLLGSVIFVYFIDPHVHR--KDSRVFLKGGVTA 198
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 57 IASNRPH-QPIYLLGNLAADLFAV--AYLFLMHTGPTARLSLEGWFLRQGLDT 113

QY 199 SPTASVGLFLTAIARYISHRPLAYKRIIVTRPKAVAFCLMWTIAIVAVLPLGWNCE 258
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 114 SLTASVATLAAIAVERHSVMAQLHSL-PRGEVMLIVGVVVAALGILGLPAHSHWL 172

QY 259 KLASVCSDDIPPHIDETLMFVIGVTSVLLLFIVVAYMYILKHAHSHAVRMIOGTQKSI 318
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 173 CALDRCSMAPLLSRSLAVW--ALSLLVFLMVAVT--RIPFYVRRVQRMAE---- 224

QY 319 IHTSDEGKVQVTRPDQARMAIRLAKTLVLLVLLIICWGLLAIMVYDVFGKKNLIKTV 378
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 225 -HVS-----CHPRYRETTLSLVKTVIILGAPVWCWTPQGVVLLDGLGCSNCVLAV 276

QY 379 FAFCSMLCLNSTVNPILYALRSKDLRHAFRSM 411
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 277 EKYFLLAEANSLVNAAVISCRDAEMRTFRRL 309

RESULT 10
US-11-110-274-6
; Sequence 6, Application US/11110274
; Publication No. US20050266502A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; TITLE OF INVENTION: Methods, Compositions and Compound Assays for Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,697-A USA
; CURRENT APPLICATION NUMBER: US/11/110,274
; CURRENT FILING DATE: 2005-04-20
; PRIOR APPLICATION NUMBER: US 60/563,661
; PRIOR FILING DATE: 2004-04-20
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 6
; LENGTH: 334
; TYPE: PR1
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-11-110-274-6

Query Match 12.8%; Score 310.5; DB 7; Length 334;
Best Local Similarity 26.9%; Pred. No. 1.5e-19;
Matches 83; Conservative 62; Mismatches 115; Indels 49; Gaps 9;

; APPLICANT: Nusser, Nora
; TITLE OF INVENTION: LPA RECEPTOR AGONISTS AND ANTAGONISTS AND METHODS OF
; TITLE OF INVENTION: USE
; FILE REFERENCE: 20609/305
; CURRENT APPLICATION NUMBER: US/11/067,884
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 60/190,370
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 09/811,838
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 4
; LENGTH: 351
; TYPE: PR1
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-11-067-884-4

Query Match 12.9%; Score 311.5; DB 7; Length 351;
Best Local Similarity 27.0%; Pred. No. 1.3e-19;
Matches 90; Conservative 60; Mismatches 150; Indels 33; Gaps 10;

QY 81 FYNKLSFKEBENIQCFMDFMVLNPSQQLAIAVLSLTGFTVLENLVLGV 140
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 8 YNETIGFFYNSGK-----ELSHWRPKDQVVVA-LGLTVSLVLLTNLAVIA 56

QY 141 ILHSRLRCPSTHPTGSLAVADLLGSVIFVYFIDPHVHR--KDSRVFLKGGVTA 198
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 57 IASNRPH-QPIYLLGNLAADLFAV--AYLFLMHTGPTARLSLEGWFLRQGLDT 113

QY 199 SPTASVGLFLTAIARYISHRPLAYKRIIVTRPKAVAFCLMWTIAIVAVLPLGWNCE 258
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 114 SLTASVATLAAIAVERHSVMAQLHSL-PRGEVMLIVGVVVAALGILGLPAHSHWL 172

QY 259 KLASVCSDDIPPHIDETLMFVIGVTSVLLLFIVVAYMYILKHAHSHAVRMIOGTQKSI 318
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 173 CALDRCSMAPLLSRSLAVW--ALSLLVFLMVAVT--RIPFYVRRVQRMAE---- 224

QY 319 IHTSDEGKVQVTRPDQARMAIRLAKTLVLLVLLIICWGLLAIMVYDVFGKKNLIKTV 378
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 225 -HVS-----CHPRYRETTLSLVKTVIILGAPVWCWTPQGVVLLDGLGCSNCVLAV 276

QY 379 FAFCSMLCLNSTVNPILYALRSKDLRHAFRSM 411
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 277 EKYFLLAEANSLVNAAVISCRDAEMRTFRRL 309

RESULT 10
US-11-110-274-6
; Sequence 6, Application US/11110274
; Publication No. US20050266502A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; TITLE OF INVENTION: Methods, Compositions and Compound Assays for Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,697-A USA
; CURRENT APPLICATION NUMBER: US/11/110,274
; CURRENT FILING DATE: 2005-04-20
; PRIOR APPLICATION NUMBER: US 60/563,661
; PRIOR FILING DATE: 2004-04-20
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 6
; LENGTH: 334
; TYPE: PR1
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-11-110-274-6

Query Match 12.8%; Score 310.5; DB 7; Length 334;
Best Local Similarity 26.9%; Pred. No. 1.5e-19;
Matches 83; Conservative 62; Mismatches 115; Indels 49; Gaps 9;

; APPLICANT: Nusser, Nora
; TITLE OF INVENTION: LPA RECEPTOR AGONISTS AND ANTAGONISTS AND METHODS OF
; TITLE OF INVENTION: USE
; FILE REFERENCE: 20609/305
; CURRENT APPLICATION NUMBER: US/11/067,884
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 60/190,370
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 09/811,838
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 4
; LENGTH: 351
; TYPE: PR1
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-11-067-884-4

Query Match 12.9%; Score 311.5; DB 7; Length 351;
Best Local Similarity 27.0%; Pred. No. 1.3e-19;
Matches 90; Conservative 60; Mismatches 150; Indels 33; Gaps 10;

QY 81 FYNKLSFKEBENIQCFMDFMVLNPSQQLAIAVLSLTGFTVLENLVLGV 140
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 8 YNETIGFFYNSGK-----ELSHWRPKDQVVVA-LGLTVSLVLLTNLAVIA 56

QY 141 ILHSRLRCPSTHPTGSLAVADLLGSVIFVYFIDPHVHR--KDSRVFLKGGVTA 198
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 57 IASNRPH-QPIYLLGNLAADLFAV--AYLFLMHTGPTARLSLEGWFLRQGLDT 113

QY 199 SPTASVGLFLTAIARYISHRPLAYKRIIVTRPKAVAFCLMWTIAIVAVLPLGWNCE 258
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 114 SLTASVATLAAIAVERHSVMAQLHSL-PRGEVMLIVGVVVAALGILGLPAHSHWL 172

QY 259 KLASVCSDDIPPHIDETLMFVIGVTSVLLLFIVVAYMYILKHAHSHAVRMIOGTQKSI 318
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 173 CALDRCSMAPLLSRSLAVW--ALSLLVFLMVAVT--RIPFYVRRVQRMAE---- 224

QY 319 IHTSDEGKVQVTRPDQARMAIRLAKTLVLLVLLIICWGLLAIMVYDVFGKKNLIKTV 378
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Db 225 -HVS-----CHPRYRETTLSLVKTVIILGAPVWCWTPQGVVLLDGLGCSNCVLAV 276

QY 379 FAFCSMLCLNSTVNPILYALRSKDLRHAFRSM 411
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 277 EKYFLLAEANSLVNAAVISCRDAEMRTFRRL 309

RESULT 10
US-11-110-274-6
; Sequence 6, Application US/11110274
; Publication No. US20050266502A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; TITLE OF INVENTION: Methods, Compositions and Compound Assays for Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,697-A USA
; CURRENT APPLICATION NUMBER: US/11/110,274
; CURRENT FILING DATE: 2005-04-20
; PRIOR APPLICATION NUMBER: US 60/563,661
; PRIOR FILING DATE: 2004-04-20
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 4
; LENGTH: 330
; TYPE: PR1
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-11-110-274-6

Query Match 11.9%; Score 289; DB 7; Length 330;
Best Local Similarity 27.8%; Pred. No. 1e-17;
Matches 89; Conservative 61; Mismatches 140; Indels 30; Gaps 12;

QY 113 PSQOLAIAVLSLTGFTVLENLVLGVLSRLRCPSTHPTGSLAVADLLGSVIFVY 172
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Db 38 PPKAWDVLCIS-GTLVSCENALVVAIVGTAFRA-PMFLLVGLSVAADLLAGLGLV 95

QY 173 SFIDFVHRKDSRVNVLKGGVTSFTASVGSFLTAIARYISHRPLAYKRIIVTRPK 232
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 96 HFAAVFCI---GSAEMSLVGVLVAMAPTASIGSLAITVDYRLSLYNALTYSETTVTR 152

QY 233 AVFAVCLMWTIAIVAVLPLGWNCEKLSQVCSDDIPPHIDETLMFVIGVTSVLLLFVY 292
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 153 TYVMALVWGGALGLGLPLVLANCLDGLTTCGVVYV-LSKNHL-----VLAIAFAFMVF 206

QY 293 AYMYILKHAHSHAVRMIOGTQK-SIIHTSDEGKVQVTRPDQARMAIRLAKTLVLIV 351
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Db 207 G---IMQLVAQICRIVCRHAQIALQRIHLLPASHYVATRKGA-----TLAVILGA 255

QY 352 LIICWGLLAIMVYDVFGKKNLIKTVFAPCSML-CLLNSTVNPILYALRSKDLRHAFRS 410
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 256 FAACW---LPFTVYCLLGDAHS--PPLYTYLTLLPATYNSMINPIIYAFNRQDVQKVLWA 310
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QY 411 MFPSCEGTQAPLDNSMGDS 430
Db 311 VCCCCSSKIPP-RSRSPD 329

RESULT 12
US-11-127-877-51
; Sequence 51, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merckhiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 51
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-127-877-51

Query Match 11.7%; Score 283; DB 7; Length 429;
Best Local Similarity 26.2%; Pred. No. 4.7e-17;
Matches 95; Conservative 72; Mismatches 156; Indels 40; Gaps 12;

QY 111 LNPSQOLAIAVLSLTGTTFTVLENLVLVCVILHSRLCRPSYHFIGSLAVAD-LLGSVI 169
Db 21 VNISKAILLGVILGGLILFGVLGNILVILSVACHRHLLH-SVTHYYIVNLAVADLLLTSTV 79

QY 170 FVYSFIDFHVHRKDSRNVLFLKGGV-TASFTASVGSILFTAIARYISIHRLAYKRIY 228
Db 80 LPFSAL-PEVLGYWAFGRVFCNIWAAVDVLCCTASIMGLCIISIDRYIGVSYPLRYPTIV 138

QY 229 TRPKAVAFCLMWTIAIVAVLPLLGWN--CEKLSQVCS-----DIPPHIDETVLMFW 279
Db 139 TORRGLMALLCVWALSIVISIGLFGWRQPAPEDEITICQINEEPGVLFPSALGFSYL--- 195

QY 280 IGTVSVLLFIVYAYMYILWKAHSHAVRMQR-----GTQKSIHHTSE---DGKQVQVTR 331
Db 196 ----PLAIIILVMYCRYVYVAKRESGLKSLTKDSQVTLRIHRKNAPAGGSGMASA 251

QY 332 PQQARMAIRL-----AKTLVLILVLLIICWGPLLAIWVDVFGKMKLIKTVFAPC 382
Db 252 KTKTHFSVRLKFSREKKAATLGIIVGCVFLCWLFPFLVMPIGSFPDPKPSSETVFKIV 311

QY 383 SMLCLLNSTVNPITIALRSKDLRHAFRSMFP--SCGTQAPLDNSMGDSCLHKHANNAAS 441
Db 312 FWLGYLNSCINPIIYPCSSQEFKAFQNVLRIQCLRRKQSSKHALGYT--LHPPSOAVEG 369

QY 442 VHR 444
Db 370 QHK 372

RESULT 14
US-11-110-274-5
; Sequence 5, Application US/11110274
; Publication No. US20050266502A1
; GENERAL INFORMATION:
; APPLICANT: Merckhiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,697-A USA
; CURRENT APPLICATION NUMBER: US/11/110,274
; CURRENT FILING DATE: 2005-04-20
; PRIOR APPLICATION NUMBER: US 60/563,661
; PRIOR FILING DATE: 2004-04-20
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-110-274-5

QY 411 MFPSCEGTQAPLDNSMGDS 430
Db 311 VCCCCSSKIPP-RSRSPD 329

RESULT 13
US-11-127-877-50
; Sequence 50, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merckhiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
```


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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 6, 2006, 21:01:17 ; Search time 231 Seconds
(without alignments)

1441.599 Million cell updates/sec

Title: US-10-521-420-1

Perfect score: 2424

Sequence: 1 MKSLDGLADTTFTTTDL.....TVKIAKVTMSVSTDTSAEAL 472

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2412	99.5	472	1	CNR1_HUMAN
2	2412	99.5	472	1	CNR1_PANTR
3	2412	99.5	472	2	Q4PLI4_HUMAN
4	2412	99.5	472	2	Q7ISPS_MACMU
5	2380	98.2	472	2	Q506J9_HUMAN
6	2377	98.1	471	2	Q4VBM6_HUMAN
7	2343.5	96.7	473	1	CNR1_RAT
8	2340.5	96.6	473	1	CNR1_MOUSE
9	2340.5	96.6	473	2	Q5SF33_MOUSE
10	2335	96.3	472	1	CNR1_FELCA
11	2250.5	92.8	473	1	CNR1_PORGU
12	2209.5	91.2	439	2	Q5UB37_HUMAN
13	2064.5	85.2	473	1	CNR1_TARGR
14	2031	83.8	470	2	Q80LM1_XENLA
15	1954	80.6	411	2	Q5JVL5_HUMAN
16	1805	74.5	363	2	Q6W9C6_DRYNI
17	1804	74.4	363	2	Q6W9C0_9RODE
18	1800	74.3	363	2	Q6W9C2_PEDCA
19	1799	74.2	361	2	Q6W9B8_9RODE
20	1793	74.0	363	2	Q6W9C4_GRAMU
21	1788	73.8	360	2	Q6W9D1_CASCN
22	1787.5	73.7	359	2	Q6W9B9_9RODE
23	1785.5	73.7	363	2	Q6W9B7_SPERTR
24	1785.5	73.7	364	2	Q6W9D2_APLRU
25	1779.5	73.4	362	2	Q6W9B4_ZAPPR
26	1774.5	73.2	364	2	Q6W9B6_TAMHU
27	1771.5	73.1	362	2	Q6W9B5_THOBO
28	1766.5	72.9	361	2	Q6W9C8_DIPS
29	1752	72.3	359	2	Q6W9C7_DIPS
30	1750	72.2	468	2	Q4ROX1_TETNG
31	1749.5	72.2	362	2	Q6W9C9_CHILA

32	1743	71.9	468	1	CNR1A_FUGRU	Q98894 fugu rubrip
33	1686	69.6	330	2	Q9BYI6_HUMAN	Q9BYI6 homo sapien
34	1686	69.6	330	2	Q9BFE4_MACMU	Q9BFE4 macaca mula
35	1686	69.6	330	2	Q9BFE5_ATEFU	Q9BFE5 atelea fusc
36	1681	69.3	330	2	Q9BFE2_CALGO	Q9BFE2 callimico g
37	1681	69.3	330	2	Q9BFE3_HYLCO	Q9BFE3 hylebates c
38	1674	69.1	475	2	Q7T3Q3_BRAKE	Q7T3Q3 brachydanio
39	1656	68.3	330	2	Q9BFC9_TAPIN	Q9BFC9 tapirus ind
40	1656	68.3	330	2	Q9BFF6_LOXAF	Q9BFF6 loxodonta a
41	1656	68.3	330	2	Q9BFF8_TRIMA	Q9BFF8 trichechus
42	1656	68.3	330	2	Q9BFG4_TAMTE	Q9BFG4 tamandua te
43	1655	68.3	330	2	Q9BFD0_CERSI	Q9BFD0 ceratotheri
44	1653	68.2	330	2	Q9BFD3_PIG	Q9BFD3 sus scrofa
45	1652	68.2	330	2	Q8MK91_AMBHO	Q8MK91 amblysomus

ALIGNMENTS

RESULT 1
CNR1_HUMAN STANDARD; PRT; 472 AA.
AC P21554; Q13949; Q9UNN0;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Cannabinoid receptor 1 (CB1) (CB-R) (CANN6).
GN Name=CNR1; Synonym=CNR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM LONG).
RC TISSUE=Brain stem;
RX MEDLINE=92028798; PubMed=1718258;
RA Gerard C., Mollereau C., Vassart G., Parmentier M.;
RT "Molecular cloning of a human cannabinoid receptor which is also
expressed in testis."
RL Biochem. J. 279:129-134(1991).
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORM LONG).
RC TISSUE=Brain stem;
RX MEDLINE=91088303; PubMed=2263478;
RA Gerard C., Mollereau C., Vassart G., Parmentier M.;
RT "Nucleotide sequence of a human cannabinoid receptor cDNA."
RN [3]
RP NUCLEOTIDE SEQUENCE (ISOFORMS LONG AND SHORT).
RC TISSUE=Lung;
RX MEDLINE=95181329; PubMed=7876112; DOI=10.1074/jbc.270.8.3726;
RA Shire D., Carillon D., Kaghad M., Calandra B., Rinaldi-Carmona M.,
Le Fur G., Caput D., Ferrara P.;
RT "An amino-terminal variant of the central cannabinoid receptor
resulting from alternative splicing."
RL J. Biol. Chem. 270:3726-3731(1995).
RN [4]
RP NUCLEOTIDE SEQUENCE (ISOFORM LONG).
RC TISSUE=Hippocampus;
RX MEDLINE=95181329; PubMed=7876112; DOI=10.1074/jbc.270.8.3726;
RA Shire D., Carillon D., Kaghad M., Calandra B., Rinaldi-Carmona M.,
Le Fur G., Caput D., Ferrara P.;
RT "An amino-terminal variant of the central cannabinoid receptor
resulting from alternative splicing."
RL J. Biol. Chem. 270:3726-3731(1995).
RN [5]
RP NUCLEOTIDE SEQUENCE (ISOFORM LONG).
RC TISSUE=Hippocampus;
RX MEDLINE=95181329; PubMed=7876112; DOI=10.1074/jbc.270.8.3726;
RA Shire D., Carillon D., Kaghad M., Calandra B., Rinaldi-Carmona M.,
Le Fur G., Caput D., Ferrara P.;
RT "An amino-terminal variant of the central cannabinoid receptor
resulting from alternative splicing."
RL J. Biol. Chem. 270:3726-3731(1995).
RN [6]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LONG).
RA Kopatz S.A., Aronstam R.S., Sharma S.V.;
RT "cDNA clones of human proteins involved in signal transduction
sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [7]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=22935763; PubMed=14574404; DOI=10.1038/nature02055;
RA Mungall A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashurst J.L.,
RA Wilming L., Jones M.C., Horton R., Hunt S.E., Scott C.E.,
RA Gilbert J.G.R., Clamp M.E., Bethel G., Milne S., Ainscough R.,
RA Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S.,
RA Babbage A.K., Bagguley C.L., Bailey J., Banerjee R., Barker D.J.,
RA Blakey S.F., Bates K., Beare D.M., Beasley H., Beasley O., Bird C.P.,
RA Blakely S.E., Bray-Allen S., Brook J., Brown A.J., Brown J.V.,
RA Burford D.C., Burrill W., Burton J., Carder C., Carter N.P.,
RA Chapman J.C., Clark S.Y., Clark G., Clee C.M., Clegg S., Cobley V.,
RA Collier R.E., Collins J.E., Colman L.K., Corby N.R., Coville G.J.,
RA Cullity K.M., Dhali P., Davies J., Dunn M., Earthrowl M.E.,
RA Ellington A.E., Evans K.A., Faulkner L., Francis M.D., Frankish A.,
RA Frankland J., French L., Garner P., Garnett J., Ghori M.J.,
RA Gilby L.M., Gillson C.J., Glithero R.J., Graham D.V., Grant M.,
RA Gribble S., Griffiths C., Griffiths M.N.D., Hall R., Halls K.S.,
RA Hammond S., Harley J.L., Hart E.A., Heath P.D., Heathcote R.,
RA Holmes S.J., Howden P.J., Howe K.L., Howell G.R., Huckle E.,
RA Humphray S.J., Humphries M.D., Hunt A.R., Johnson C.M., Joy A.A.,
RA Kay M., Keenan S.J., Kimberley A.M., King A., Laird G.K., Langford C.,
RA Lawlor S., Leongamornlert D.A., Leversha M., Lloyd C.R., Lloyd D.M.,
RA Laveland J.E., Lovell J., Martin S., Mashregi-Mohammadi M.,
RA Masland G.L., Matthews L., McCann O.T., McLaren S.J., McKay K.,
RA McMurray A., Moore M.J.F., Mullikin J.C., Niblett D., Nickerson T.,
RA Novik K.L., Oliver K., Overton-Larty E.K., Parker A., Patel R.,
RA Pearce A.V., Peck A.I., Phillimore B.J.C.T., Phillips S., Plumb R.W.,
RA Porter K.M., Ramsey V., Ranby S.A., Rice C.M., Ross M.T., Searle S.M.,
RA Sehra H.K., Sheridan E., Skuce C.D., Smith S., Smith M., Spreggion L.,
RA Squares S.L., Steward C.A., Symamore N., Tamlyn-Hall G., Tester J.,
RA Theaker A.J., Thomas D.W., Thorpe A., Tracey A., Tromans A., Tubby B.,
RA Wall M., Wallis J.M., West A.P., White S.S., Whitehead S.L.,
RA Whittaker H., Wild A., Willey D.J., Wilmer T.E., Wood J.M., Wray P.W.,
RA Wyatt J.C., Young L., Younger R.M., Bentley D.R., Coulson A.,
RA Durbin R., Hubbard T., Sulston J.E., Dunham I., Rogers J., Beck S.;
RT "The DNA sequence and analysis of human chromosome 6";
RL Nature 425:805-811(2003).
[8]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LONG).
RX TISSUE=Lung.
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.C., Krzywinski M.I., Skalek U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Involved in cannabinoid-induced CNS effects. Acts by
inhibiting adenylyl cyclase. Could be a receptor for anandamide.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=P21554-1; Sequence=Displayed;
CC Name=Short; Synonyms=CB1A;
CC IsoId=P21554-2; Sequence=VSP_001868;
CC -1- TISSUE SPECIFICITY: Found in all peripheral organs tested: heart,
colon, stomach, liver, pancreas, placenta, lung, kidney, bile
duct, spleen, adrenal gland, muscle, brain, and testis; and
CC

throughout the central nervous system.
-!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL Outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.

DR EMBL; X54937; CAA38699.1; -; mRNA.
DR EMBL; X81120; CAA57018.1; -; mRNA.
DR EMBL; X81121; CAA57019.1; -; mRNA.
DR EMBL; AF107262; AAD34320.1; -; mRNA.
DR EMBL; U73304; AAB18200.1; -; Genomic DNA.
DR EMBL; AY225225; AAO67710.1; -; Genomic DNA.
DR EMBL; AL136096; CAB96726.1; -; Genomic DNA.
DR EMBL; BC074811; AAH74811.1; -; mRNA.
DR EMBL; BC074812; AAH74812.1; -; mRNA.
DR PIR; S17595; S17595.
DR PDB; 1LVQ; NMR; A=338-346.
DR PDB; 1LVQ; NMR; A=338-346.
DR Ensembl; ENSG00000118432; Homo sapiens.
DR HGNC; HGNC:2159; CNR1.
DR MIM; 114610; -;
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0004949; F:cannabinoid receptor activity; TAS.
DR GO; GO:0007610; P:behavior; TAS.
DR GO; GO:0007187; P:G-protein signaling, coupled to cyclic nucl. .; TAS.
DR InterPro; IPR002230; G-protein coupled receptor.
DR InterPro; IPR000810; G-protein coupled receptor.
DR InterPro; IPR000276; GPCR Rhodopsin.
DR PANTHER; PTHR19266:SF8; G-protein coupled receptor 1.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00522; CANNABINOIDR.
DR PRINTS; PR00362; CANNABINOIDR.
DR PRINTS; PR00237; GPCR RHODOPSIN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL_1; 1.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL_2; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL_3; 1.
KW 3D-structure; Alternative splicing; G-protein coupled receptor;
KW Glycoprotein; Receptor; Transducer; Transmembrane.
FT TOPO_DOM 1 116 Extracellular (Potential).
FT TRANSMEM 117 142 1 (Potential).
FT TOPO_DOM 143 154 Cytoplasmic (Potential).
FT TRANSMEM 155 175 2 (Potential).
FT TOPO_DOM 176 187 Extracellular (Potential).
FT TRANSMEM 188 212 3 (Potential).
FT TOPO_DOM 213 232 Cytoplasmic (Potential).
FT TRANSMEM 233 255 4 (Potential).
FT TOPO_DOM 256 273 Extracellular (Potential).
FT TRANSMEM 274 299 5 (Potential).
FT TOPO_DOM 300 344 Cytoplasmic (Potential).
FT TRANSMEM 345 355 6 (Potential).
FT TOPO_DOM 366 377 Extracellular (Potential).
FT TRANSMEM 378 399 7 (Potential).
FT TOPO_DOM 400 472 Cytoplasmic (Potential).
FT CARBOHYD 77 77 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 83 83 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 112 112 N-linked (GlcNAc. .) (Potential).
FT VARSPLIC 1 89 MKSLDGLADTTFTTTTLLVGSNDIQYEDIKGMASKL
GYFPQKFLTSRFGSPQKRWAGDNPQLVPAQDVNITEFY
NKSLSF -> MALQIPPSAPSLTCTWAQMTFTSKTS
(in isoform Short).
(FTId=VSP_001868).
FT CONFLICT 200 200 F -> L (in Ref. 4).
FT CONFLICT 216 216 I -> V (in Ref. 4).
FT CONFLICT 246 246 V -> A (in Ref. 4).
SQ SEQUENCE 472 AA; 52858 MW; 1D2E49061D12ABF2 CRC64;

Query Match 99.5%; Score 2412; DB 1; Length 472;
Best Local Similarity 99.6%; Pred. No. 2.8e-156;
Matches 470; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 MKSILDLGLADTTTTRITTTDLLLVGSDIOYEDIKGDMASKLGYFPQKPLTTSFRGSPFQE 60
Db 1 MKSILDLGLADTTTTRITTTDLLLVGSDIOYEDIKGDMASKLGYFPQKPLTTSFRGSPFQE 60
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Db 61 KMTAGNPQLVPADQVNITFYNKSLSSFKENEENIQCGENFMDIECFMWLNPSQQLAIA 120
QY 121 VLSLTGTFVLENLVLCVLHRSRLCRPSYHFHIGSLAVADLLGSLVIFYSFIDPHVF 180
Db 121 VLSLTGTFVLENLVLCVLHRSRLCRPSYHFHIGSLAVADLLGSLVIFYSFIDPHVF 180
QY 181 HRKDSRVNLFKLGCVTASVGSIFLTAIARYISIHRLAYKRIIVTRPKAVAFCLM 240
Db 181 HRKDSRVNLFKLGCVTASVGSIFLTAIARYISIHRLAYKRIIVTRPKAVAFCLM 240
QY 241 WTIAIVAVLPPLGWNCEKLSQVCSDFPHIDETFLMFVIGVTSVLLLFIVYAYMYILWK 300
Db 241 WTIAIVAVLPPLGWNCEKLSQVCSDFPHIDETFLMFVIGVTSVLLLFIVYAYMYILWK 300
QY 301 AHSHAVRMIOGTOKSIIHTSDEGKVQVTRPDQARMADIRLAKTLVLVLVLIICWGPLL 360
Db 301 AHSHAVRMIOGTOKSIIHTSDEGKVQVTRPDQARMADIRLAKTLVLVLVLIICWGPLL 360
QY 361 AIMVYDVFQKMKLIKTVFAFCMLCLNSTVNPPIIYALRSKDLRHAFRSMFSCETAQ 420
Db 361 AIMVYDVFQKMKLIKTVFAFCMLCLNSTVNPPIIYALRSKDLRHAFRSMFSCETAQ 420
QY 421 PLNSMGSDSCLHGHANNAASVHRAESCIKSTVKIAKVTMSVSTDTSAEAL 472
Db 421 PLNSMGSDSCLHGHANNAASVHRAESCIKSTVKIAKVTMSVSTDTSAEAL 472

RESULT 2
CNRI_PANTH
ID_CNRI_PANTH STANDARD; PRT; 472 AA.
AC Q51S73; 2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Cannabinoid receptor 1 (CB1) (CB-R).
GN Name=CNRI;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
-OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pan.
OC NCBI_TaxID=9598;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX PubMed=15620360; DOI=10.1016/j.j.cell.2004.11.040;
RA Dorus S., Vallerend E.J., Evans P.D., Anderson J.R., Gilbert S.L.,
RA Mahowald M., Wyckoff G.J., Malcom C.M., Lahn B.T.;
RT "Accelerated evolution of nervous system genes in the origin of Homo sapiens.";
RL Cell 119:1027-1040(2004).
CC -!- FUNCTION: Involved in cannabinoid-induced CNS effects. Acts by inhibiting adenylylate cyclase. Could be a receptor for anandamide (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC -----
CC EMBL; AY665255; AAV74293.1; -; mRNA.
DR InterPro; IPR002230; Cnbdoid_receptor.
DR InterPro; IPR000810; Cnoid_receptor1.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR PANTHER; PTHR19286:SF8; Cnoid_receptor1; 1.
DR Pfam; PF00001; 7tm_1; 1.
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DR PRINTS; PR00522; CANNABINOIDIR.
DR PRINTS; PR00362; CANNABINOIDIR.
DR PRINTS; PR00237; GPCRRHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transducer; Transmembrane.
KW TOPO_DOM 1 116 Extracellular (Potential).
FT TRANSMEM 117 142 1 (Potential).
FT TOPO_DOM 143 154 Cytoplasmic (Potential).
FT TRANSMEM 155 175 2 (Potential).
FT TOPO_DOM 176 187 Extracellular (Potential).
FT TRANSMEM 188 212 3 (Potential).
FT TOPO_DOM 213 232 Cytoplasmic (Potential).
FT TRANSMEM 233 255 4 (Potential).
FT TOPO_DOM 256 273 Extracellular (Potential).
FT TRANSMEM 274 299 5 (Potential).
FT TOPO_DOM 300 344 Cytoplasmic (Potential).
FT TRANSMEM 345 365 6 (Potential).
FT TOPO_DOM 366 377 Extracellular (Potential).
FT TRANSMEM 378 399 7 (Potential).
FT TOPO_DOM 400 472 Cytoplasmic (Potential).
FT CARBOHYD 77 77 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 83 83 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 472 AA; 52858 MW; 1D2E49061D12ABF2 CRC64;
Query Match 99.5%; Score 2412; DB 1; Length 472;
Best Local Similarity 99.6%; Pred. No. 2.8e-156;
Matches 470; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MKSILDLGLADTTTTRITTTDLLLVGSDIOYEDIKGDMASKLGYFPQKPLTTSFRGSPFQE 60
Db 1 MKSILDLGLADTTTTRITTTDLLLVGSDIOYEDIKGDMASKLGYFPQKPLTTSFRGSPFQE 60
QY 61 KMTAGNPQLVPADQVNITFYNKSLSSFKENEENIQCGENFMDIECFMWLNPSQQLAIA 120
Db 61 KMTAGNPQLVPADQVNITFYNKSLSSFKENEENIQCGENFMDIECFMWLNPSQQLAIA 120
QY 121 VLSLTGTFVLENLVLCVLHRSRLCRPSYHFHIGSLAVADLLGSLVIFYSFIDPHVF 180
Db 121 VLSLTGTFVLENLVLCVLHRSRLCRPSYHFHIGSLAVADLLGSLVIFYSFIDPHVF 180
QY 181 HRKDSRVNLFKLGCVTASVGSIFLTAIARYISIHRLAYKRIIVTRPKAVAFCLM 240
Db 181 HRKDSRVNLFKLGCVTASVGSIFLTAIARYISIHRLAYKRIIVTRPKAVAFCLM 240
QY 241 WTIAIVAVLPPLGWNCEKLSQVCSDFPHIDETFLMFVIGVTSVLLLFIVYAYMYILWK 300
Db 241 WTIAIVAVLPPLGWNCEKLSQVCSDFPHIDETFLMFVIGVTSVLLLFIVYAYMYILWK 300
QY 301 AHSHAVRMIOGTOKSIIHTSDEGKVQVTRPDQARMADIRLAKTLVLVLVLIICWGPLL 360
Db 301 AHSHAVRMIOGTOKSIIHTSDEGKVQVTRPDQARMADIRLAKTLVLVLVLIICWGPLL 360
QY 361 AIMVYDVFQKMKLIKTVFAFCMLCLNSTVNPPIIYALRSKDLRHAFRSMFSCETAQ 420
Db 361 AIMVYDVFQKMKLIKTVFAFCMLCLNSTVNPPIIYALRSKDLRHAFRSMFSCETAQ 420
QY 421 PLNSMGSDSCLHGHANNAASVHRAESCIKSTVKIAKVTMSVSTDTSAEAL 472
Db 421 PLNSMGSDSCLHGHANNAASVHRAESCIKSTVKIAKVTMSVSTDTSAEAL 472

RESULT 3
Q4PLI4 HUMAN
ID_Q4PLI4 HUMAN PRELIMINARY; PRT; 472 AA.
AC Q4PLI4;
DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE Cannabinoid receptor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain tumor;
RA Kumar S., Gupta S., Shabana, Sharmila, Sharma G.;
DR Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -l- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR EMBL: DQ067455; AY68486.1; -; mRNA.
DR InterPro: IPR002230; Cnoid_receptor.
DR InterPro: IPR000810; Cnoid_receptor1.
DR Pfam: PF00001; 7tm 1; 1.
DR PRINTS: PR00522; CANABINOIDIR.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PRINTS: PR00362; CANNABINOIDR.
DR PROSITE: PS00237; G-PROTEIN RECP F1_1; UNKNOWN 1.
DR PROSITE: PS0262; G-PROTEIN RECP F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 472 AA; 52858 MW; 1D2B49061D12A8F2 CRC64;

Query Match 99.5%; Score 2412; DB 2; Length 472;
Best Local Similarity 99.6%; Pred. No. 2.8e-156;
Matches 470; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKSILDLGLADTTFRITTTDLLVVGSDIOYEDIKGMASKLGVFPKPLTSFRGSPFOE 60
DB 1 MKSILDLGLADTTFRITTTDLLVVGSDIOYEDIKGMASKLGVFPKPLTSFRGSPFOE 60

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DB 61 KMTAGNPOLVPADQVNITEFYFKSLSSFKENEENIQCGENFMDIECFVNLNPSQOLAIA 120

QY 121 VLSLTGLTFTVLNLLVLCVILHRSRLCRPSYHFHFGSLAVADLLGSLVFVYSFIDFHFV 180
DB 121 VLSLTGLTFTVLNLLVLCVILHRSRLCRPSYHFHFGSLAVADLLGSLVFVYSFIDFHFV 180

QY 181 HRKDSRNVELFKLGGVTASFTASVGLFTATARYISIHRLAYKRIIVTRPKAVAFCLM 240
DB 181 HRKDSRNVELFKLGGVTASFTASVGLFTATARYISIHRLAYKRIIVTRPKAVAFCLM 240

QY 241 WTIAIVIAVPLPLGNCEKLSQVCSDFPHIDETVLMFWIGVTSVLLLFIVVAYMYLWK 300
DB 241 WTIAIVIAVPLPLGNCEKLSQVCSDFPHIDETVLMFWIGVTSVLLLFIVVAYMYLWK 300

QY 301 AHSNAVMIQRGTQKSIITHTSEDGKVQVTRPDQARMALRLAKTLVLILVLLICWGPLL 360
DB 301 AHSNAVMIQRGTQKSIITHTSEDGKVQVTRPDQARMALRLAKTLVLILVLLICWGPLL 360

QY 361 AIMVYDVFGGMNKLKTVFAFCMLCLNLTNPPIIYALRSKDLRHAFRSMPPSCSGTAQ 420
DB 361 AIMVYDVFGGMNKLKTVFAFCMLCLNLTNPPIIYALRSKDLRHAFRSMPPSCSGTAQ 420

QY 421 PLDMSGDSCLHKKHANNAAHVRAAESCIKSTVKIAKVTMSVSTDTSAEAL 472
DB 421 PLDMSGDSCLHKKHANNAAHVRAAESCIKSTVKIAKVTMSVSTDTSAEAL 472

RESULT 4
Q71SP5_MACMU
ID Q71SP5_MACMU PRELIMINARY; PRT; 472 AA.
AC Q71SP5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cannabinoid receptor CB-1.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;
OC Cercopitheciidae; Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Cerebellum;
RA Miller G.M., Madras B.K.;
DR Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -l- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR EMBL: AF286025; AAP97250.1; -; mRNA.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0004949; F:cannabinoid receptor activity; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR GO: GO:0007165; P:signal transduction; IEA.
DR InterPro: IPR002230; Cnoid_receptor.
DR InterPro: IPR000810; Cnoid_receptor1.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm 1; 1.
DR PRINTS: PR00522; CANABINOIDIR.
DR PRINTS: PR00362; CANNABINOIDR.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G-PROTEIN RECP F1_1; UNKNOWN 1.
DR PROSITE: PS0262; G-PROTEIN RECP F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 472 AA; 52858 MW; 1D2E49061D12ABF2 CRC64;

Query Match 99.5%; Score 2412; DB 2; Length 472;
Best Local Similarity 99.6%; Pred. No. 2.8e-156;
Matches 470; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKSILDLGLADTTFRITTTDLLVVGSDIOYEDIKGMASKLGVFPKPLTSFRGSPFOE 60
DB 1 MKSILDLGLADTTFRITTTDLLVVGSDIOYEDIKGMASKLGVFPKPLTSFRGSPFOE 60

QY 61 KMTAGNPOLVPADQVNITEFYFKSLSSFKENEENIQCGENFMDIECFVNLNPSQOLAIA 120
DB 61 KMTAGNPOLVPADQVNITEFYFKSLSSFKENEENIQCGENFMDIECFVNLNPSQOLAIA 120

QY 121 VLSLTGLTFTVLNLLVLCVILHRSRLCRPSYHFHFGSLAVADLLGSLVFVYSFIDFHFV 180
DB 121 VLSLTGLTFTVLNLLVLCVILHRSRLCRPSYHFHFGSLAVADLLGSLVFVYSFIDFHFV 180

QY 181 HRKDSRNVELFKLGGVTASFTASVGLFTATARYISIHRLAYKRIIVTRPKAVAFCLM 240
DB 181 HRKDSRNVELFKLGGVTASFTASVGLFTATARYISIHRLAYKRIIVTRPKAVAFCLM 240

QY 241 WTIAIVIAVPLPLGNCEKLSQVCSDFPHIDETVLMFWIGVTSVLLLFIVVAYMYLWK 300
DB 241 WTIAIVIAVPLPLGNCEKLSQVCSDFPHIDETVLMFWIGVTSVLLLFIVVAYMYLWK 300

QY 301 AHSNAVMIQRGTQKSIITHTSEDGKVQVTRPDQARMALRLAKTLVLILVLLICWGPLL 360
DB 301 AHSNAVMIQRGTQKSIITHTSEDGKVQVTRPDQARMALRLAKTLVLILVLLICWGPLL 360

QY 361 AIMVYDVFGGMNKLKTVFAFCMLCLNLTNPPIIYALRSKDLRHAFRSMPPSCSGTAQ 420
DB 361 AIMVYDVFGGMNKLKTVFAFCMLCLNLTNPPIIYALRSKDLRHAFRSMPPSCSGTAQ 420

QY 421 PLDMSGDSCLHKKHANNAAHVRAAESCIKSTVKIAKVTMSVSTDTSAEAL 472
DB 421 PLDMSGDSCLHKKHANNAAHVRAAESCIKSTVKIAKVTMSVSTDTSAEAL 472

RESULT 5
Q506J9_HUMAN
ID Q506J9_HUMAN PRELIMINARY; PRT; 472 AA.
AC Q506J9;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Cannabinoid receptor type-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;


```

RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Brain tumor;
RA Kumar S., Gupta S., Kariath A., Sharma G.;
RA Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
RC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
RL EMBL; AY95204; AA211179.1; -; mRNA.
DR GO; GO:0004872; F-receptor activity; IEA.
DR GO; GO:002230; G-protein coupled receptor.
DR InterPro; IPR000810; GPCR_Rhodopsin.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00522; CANABINOID1R.
DR PRINTS; PR00362; CANABINOIDR.
DR PRINTS; PR00237; GPCR_Rhodopsin.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS00262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 472 AA; 52628 MW; 49389F3C2C8CC10F CRC64;

Query Match 98.2%; Score 2380; DB 2; Length 472;
Best Local Similarity 98.5%; Pred. No. 4.3e-154;
Matches 465; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MKSLDGLADTTFTTTTDLVYGSNDIQYEDIKGDMASKLGYPPQKPLTSFRGSPFOE 60
Db 1 MKSLDGLADTTFTTTTDLVYGSNDIQYEDIKGDMASKLGYPPQKPLTSFRGSPFOE 60

Qy 61 KMTAGDNFQLPADQVNITEFYKSLSSFKENEENIQCGENFMDIECFMVLNPSQQLAIA 120
Db 61 KMTAGDNFQLPADQVNITEFYKSLSSFKENEENIQCGENFMDIECFMVLNPSQQLAIA 120

Qy 121 VLSLTGLTFTVLENLVLCVILHSRLCRPSYHFIGSLAVADLLGSVIFVYSFIDFHFV 180
Db 121 VLSLTGLTFTVLENLVLCVILHSRLCRPSYHFIGSLAVADLLGSVIFVYSFIDFHFV 180

Qy 181 HRKDSRNVPFLKGGVTSFTASVGSFLTAIARYISIHRLAYKRVITRPAKVAFLMW 240
Db 181 HRKDSRNVPFLKGGVTSFTASVGSFLTAIARYISIHRLAYKRVITRPAKVAFLMW 240

Qy 241 WTIAIVAVPLLGWNCCKLQSVCSIDIPPHIDETVLMFWIGVTSVLLLFIVYAYMYLWK 300
Db 241 WTIAIVAVPLLGWNCCKLQSVCSIDIPPHIDETVLMFWIGVTSVLLLFIVYAYMYLWK 300

Qy 301 AHSNAVMIQRGTQKSIITHTSEDKGVQVTRPDQARMAIRLAKTLVILVLIICWGPLL 360
Db 301 AHSNAVMIQRGTQKSIITHTSEDKGVQVTRPDQARMAIRLAKTLVILVLIICWGPLL 360

Qy 361 AIMVYDFGKMKLIKTVAFCSMLCLLNTVNPPIIYALRSKDLRHAFRSPFSGGTAQ 420
Db 361 AIMVYDFGKMKLIKTVAFCSMLCLLNTVNPPIIYALRSKDLRHAFRSPFSGGTAQ 420

Qy 421 PLDMSMGSDCLHKHANNAAVHRAAESCIKSTVKIAKVTMSVSTDSAEAL 472
Db 421 PLDMSMGSDCLHKHANNAAVHRAAESCIKSTVKIAKVTMSVSTDSAEAL 472

RESULT 6
Q4VB6_HUMAN
ID Q4VB6_HUMAN PRELIMINARY; PRT; 471 AA.
AC Q4VB6;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE CNR1 protein (Fragment).
GN Name=CNR1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP NUCLEOTIDE SEQUENCE.

```

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RC TISSUE=G-protein coupled receptors;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.B.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., and
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=G-protein coupled receptors;
RG NIH MGC Project;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC095513; AA95513.1; -; mRNA.
DR InterPro; IPR002230; G-protein coupled receptor.
DR InterPro; IPR000810; G-protein coupled receptor.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00522; CANABINOID1R.
DR PRINTS; PR00362; CANABINOIDR.
DR PRINTS; PR00237; GPCR_Rhodopsin.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS00262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
FT NON_TER 1
FT NON_TER 471
SQ SEQUENCE 471 AA; 52674 MW; 51DC852E2E43DD10 CRC64;

Query Match 98.1%; Score 2377; DB 2; Length 471;
Best Local Similarity 98.7%; Pred. No. 6.9e-154;
Matches 465; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 KSILDLADTTFTTTTDLVYGSNDIQYEDIKGDMASKLGYPPQKPLTSFRGSPFOE 61
Db 1 KSILDLADTTFTTTTDLVYGSNDIQYEDIKGDMASKLGYPPQKPLTSFRGSPFOE 60

Qy 62 MTAGDNFQLPADQVNITEFYKSLSSFKENEENIQCGENFMDIECFMVLNPSQQLAIA 121
Db 61 MTAGDNFQLPADQVNITEFYKSLSSFKENEENIQCGENFMDIECFMVLNPSQQLAIA 120

Qy 122 LSLTLGTFTVLENLVLCVILHSRLCRPSYHFIGSLAVADLLGSVIFVYSFIDFHFV 181
Db 121 LSLTLGTFTVLENLVLCVILHSRLCRPSYHFIGSLAVADLLGSVIFVYSFIDFHFV 180

Qy 182 RKDSRNVPFLKGGVTSFTASVGSFLTAIARYISIHRLAYKRVITRPAKVAFLMW 241
Db 181 RKDSRNVPFLKGGVTSFTASVGSFLTAIARYISIHRLAYKRVITRPAKVAFLMW 240

Qy 242 TIAIVAVPLLGWNCCKLQSVCSIDIPPHIDETVLMFWIGVTSVLLLFIVYAYMYLWK 301
Db 241 TIAIVAVPLLGWNCCKLQSVCSIDIPPHIDETVLMFWIGVTSVLLLFIVYAYMYLWK 300

Qy 302 HSHAVMIQRGTQKSIITHTSEDKGVQVTRPDQARMAIRLAKTLVILVLIICWGPLL 361
Db 301 HSHAVMIQRGTQKSIITHTSEDKGVQVTRPDQARMAIRLAKTLVILVLIICWGPLL 360

Qy 362 IMVYDFGKMKLIKTVAFCSMLCLLNTVNPPIIYALRSKDLRHAFRSPFSGGTAQ 421
Db 361 IMVYDFGKMKLIKTVAFCSMLCLLNTVNPPIIYALRSKDLRHAFRSPFSGGTAQ 420

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QY 422 LNSMGSDSCLHKNNAASVHRAAESCIKSTVKIAKVTMSVSTDSAEAL 472
 |||||
 Db 421 LNSMGSDSCLHKNNAASVHRAAESCIKSTVKIAKVTMSVSTDSAEAL 471

RESULT 7
 CNR1_RAT
 ID CNR1_RAT STANDARD; PRT; 473 AA.
 AC P20272;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Cannabinoid receptor 1 (CB1) (CB-R) (Brain-type cannabinoid receptor).
 DN Name=Cnr1; Synonyms=Skr6;
 GN Rattus norvegicus (Rat).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=101116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain cortex;
 RX MEDLINE=90332039; PubMed=2165569; DOI=10.1038/346561a0;
 RA Matsuda L.A., Lolait S.J., Brownstein M.J., Young A.C., Bonner T.I.;
 RT "Structure of a cannabinoid receptor and functional expression of the
 RT cloned cDNA";
 RL Nature 346:561-564 (1990).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=96429553; PubMed=8832654; DOI=10.1016/0304-3940(96)12792-0;
 RA Ho B.Y., Zhao J.;
 RT "Determination of the cannabinoid receptors in mouse x rat hybridoma
 RT Ng108-15 cells and rat GH4C1 cells.";
 RL Neurosci. Lett. 212:123-126 (1996).
 RN [3]
 RP NUCLEOTIDE SEQUENCE OF 1-107.
 RX MEDLINE=95181329; PubMed=7876112; DOI=10.1074/jbc.270.8.3726;
 RA Shire D., Carillon C., Kaghad M., Calandra B., Rinaldi-Carmona M.,
 RA Le Fur G., Caput D., Ferrara P.;
 RT "An amino-terminal variant of the central cannabinoid receptor
 RT resulting from alternative splicing.";
 RL J. Biol. Chem. 270:3726-3731 (1995).
 CC -|- FUNCTION: Involved in cannabinoid-induced CNS effects. Acts by
 CC inhibiting adenylyl cyclase. Could be a receptor for anandamide.
 CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -|- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; X55812; CA393332.1; -; mRNA.
 DR EMBL; U40395; AAA99067.1; -; mRNA.
 DR FIR; A33117; A33117.
 DR Ensemble; ENSRNOG0000008223; Rattus norvegicus.
 DR RGD; 2369; Cnr1.
 DR InterPro; IPR002230; Cbnoid receptor.
 DR InterPro; IPR000810; GPCR_Rhodopsin.
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR PANTHER; PTHR19266:SF8; Cnoid_receptor1; 1.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00522; CANNABINOIDR.
 DR PRINTS; PR00362; CANNABINOIDR.
 DR PRINTS; PR00237; GPCR_RHOOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Receptor; Transducer;
 KW Transmembrane.
 FT TOPO_DOM 1 117 Extracellular (Potential).
 FT TRANSMEM 118 143 1 (Potential).

FT TOPO_DOM 144 155 Cytoplasmic (Potential).
 FT TRANSMEM 156 176 2 (Potential).
 FT TOPO_DOM 177 188 Extracellular (Potential).
 FT TRANSMEM 189 213 3 (Potential).
 FT TOPO_DOM 214 233 Cytoplasmic (Potential).
 FT TRANSMEM 234 256 4 (Potential).
 FT TOPO_DOM 257 274 Extracellular (Potential).
 FT TRANSMEM 275 300 5 (Potential).
 FT TOPO_DOM 301 345 Cytoplasmic (Potential).
 FT TRANSMEM 346 366 6 (Potential).
 FT TOPO_DOM 367 378 Extracellular (Potential).
 FT TRANSMEM 379 400 7 (Potential).
 FT TOPO_DOM 401 473 Cytoplasmic (Potential).
 FT CARBOHYD 78 78 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 84 84 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 473 AA; 52845 MW; E59A66AFE17B646C CRC64;

Query Match 96.7%; Score 2343.5; DB 1; Length 473;
 Best Local Similarity 96.8%; Pred. No. 1.3e-151;
 Matches 458; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

QY 1 MKSIIDGLADTTFTTTDLYVGSNDIQYEDIKGDMSKLGYPQKPELTSPRGSPFOR 60
 |||||
 Db 1 MKSIIDGLADTTFTTTDLYVGSNDIQYEDIKGDMSKLGYPQKPELTSPRGSPFOR 60
 |||||
 QY 61 KMTAGDNPOLVPA-DOVNITEFYNKSLGSFKENEENIOCGENFMDECEPMVLNPSQOLAI 119
 |||||
 Db 61 KMTAGDNPLVPAGDTTITEFYNKSLGSFKENEENIOCGENFMDECEPMVLNPSQOLAI 120
 |||||
 QY 120 AVLSTLTGTTVLENLVLCVILHSRLCRPSYHFIGSLAVADLLGSVIFYSFIDFHV 179
 |||||
 Db 121 AVLSTLTGTTVLENLVLCVILHSRLCRPSYHFIGSLAVADLLGSVIFYSFIDFHV 180
 |||||
 QY 180 FIRKSRNVFLKLGVTASTASVGSLEFLTAIAYISIHRLAYKRIYTRKAVVAFCL 239
 |||||
 Db 181 FHRKDSPNVFLKLGVTASTASVGSLEFLTAIDRIYISIHRLAYKRIYTRKAVVAFCL 240
 |||||
 QY 240 MWTIAIVAVLPLLGWCKQLQSCSDIPPHIDETVLMFWIGVTSVLLLFIVVAYWILW 299
 |||||
 Db 241 MWTIAIVAVLPLLGWCKQLQSCSDIPPLIDETVLMFWIGVTSVLLLFIVVAYWILW 300
 |||||
 QY 300 KAHSHAVRMIOQTQKSIHHTSEDKGVQVTPDQARMAIRLAKTLVLVLVLIICWGPL 359
 |||||
 Db 301 KAHSHAVRMIOQTQKSIHHTSEDKGVQVTPDQARMDIRLAKTLVLVLVLIICWGPL 360
 |||||
 QY 360 LAIMYDYVFGKMKLIKTVFAFCSMLCLNLTNVNPIIYALRSKDLRHAFRSPFCEGTA 419
 |||||
 Db 361 LAIMYDYVFGKMKLIKTVFAFCSMLCLNLTNVNPIIYALRSKDLRHAFRSPFCEGTA 420
 |||||
 QY 420 QPLDNSMGSDSCLHKNNAASVHRAAESCIKSTVKIAKVTMSVSTDSAEAL 472
 |||||
 Db 421 QPLDNSMGSDSCLHKNNAASVHRAAESCIKSTVKIAKVTMSVSTDSAEAL 473
 |||||

RESULT 8
 CNR1_MOUSE
 ID CNR1_MOUSE STANDARD; PRT; 473 AA.
 AC P47746;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Cannabinoid receptor 1 (CB1) (CB-R) (Brain-type cannabinoid receptor).
 DN Name=Cnr1;
 GN Mus musculus (Mouse).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=96272305; PubMed=8777318;
 RA Chakrabarti A., Onaivi E.S., Chaudhuri G.;

RT "Cloning and sequencing of a cDNA encoding the mouse brain-type
 RT cannabinoid receptor protein.";
 RL DNA Seq. 5:385-388(1995).
 RN [2]
 RC NUCLEOTIDE SEQUENCE.
 RP Bonner T.I.;
 RA Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 RL [3]
 RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE=96429553; PubMed=8832654; DOI=10.1016/0304-3940(96)12792-0;
 RA Ho B.Y., Zhao J.;
 RT "Determination of the cannabinoid receptors in mouse x rat hybridoma
 RT NG108-15 cells and rat GH4C1 cells.";
 RL Neurosci. Lett. 212:123-126(1996).
 RN [4]
 RN NUCLEOTIDE SEQUENCE.
 RP Yuan Z.-Q., Li L., Qiu B.-S., Song D.-K.;
 RA "cDNA cloning and expression analysis of mouse cannabinoid receptor
 RT (CB1) gene.";
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=129/Sv;
 RC MEDLINE=9910599; PubMed=9888857; DOI=10.1126/science.283.5400.401;
 RA Ledent C., Valverde O., Cossu G., Petitot F., Aubert J.F., Beslot F.,
 RA Boehme G.A., Imperato A., Pedrazzini T., Roques B.P., Vassart G.,
 RA Fratta W., Parmentier M.;
 RT "Unresponsiveness to cannabinoids and reduced addictive effects of
 RT opiates in CB1 receptor knockout mice.";
 RL Science 283:401-404(1999).
 RN [6]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RP STRAIN=C57BL/6; TISSUE=Brain;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan T., Moore T., Max S.I., Wang J.M., Hong L.,
 RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Involved in cannabinoid-induced CNS effects. Acts by
 CC inhibiting adenylylase cyclase. Could be a receptor for anandamide.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; U17985; AAA57202.1; -; mRNA.
 DR EMBL; U22948; AAA64413.1; -; Genomic_DNA.
 DR EMBL; UA0709; AAA91176.1; -; mRNA.
 DR EMBL; AF153345; AAD34624.1; -; mRNA.
 DR EMBL; Y18374; CAB42647.1; -; Genomic_DNA.
 DR EMBL; BC070447; AAH70447.1; -; mRNA.
 DR EMBL; BC079564; AAH79564.1; -; mRNA.

DR Ensembl; ENSMUSG00000044288; Mus musculus.
 DR MGI:104615; Cnrl.
 DR GO: GO:0016021; C: integral to membrane; TAS.
 DR InterPro; IPR002230; Cnbnoid_receptor.
 DR InterPro; IPR000810; Cnoid_receptor1.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR PANTHER; PTHR1266:SF8; Cnoid_receptor1; 1.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00522; CANNABINOIDIR.
 DR PRINTS; PR00362; CANNABINOIDS.
 DR PRINTS; PR00237; GPCR_Rhodopsn.
 DR PROSITE; PS00237; G-PROTEIN_RECPT_F1_1; 1.
 DR PROSITE; PS0262; G-PROTEIN_RECPT_F1_2; 1.
 DR G-protein coupled receptor; Glycoprotein; Receptor; Transducer;
 KW Transmembrane.
 KM FT TOPO_DOM 1 117 Extracellular (Potential).
 FT TRANSMEM 118 143 1 (Potential).
 FT TOPO_DOM 144 155 Cytoplasmic (Potential).
 FT TRANSMEM 156 176 2 (Potential).
 FT TOPO_DOM 177 188 Extracellular (Potential).
 FT TRANSMEM 189 213 3 (Potential).
 FT TOPO_DOM 214 233 Cytoplasmic (Potential).
 FT TRANSMEM 234 256 4 (Potential).
 FT TOPO_DOM 257 274 Extracellular (Potential).
 FT TRANSMEM 275 300 5 (Potential).
 FT TOPO_DOM 301 345 Cytoplasmic (Potential).
 FT TRANSMEM 346 366 6 (Potential).
 FT TOPO_DOM 367 378 Extracellular (Potential).
 FT TRANSMEM 379 400 7 (Potential).
 FT TOPO_DOM 401 473 Cytoplasmic (Potential).
 FT CARBOHYD 84 84 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 9 9 A -> G (in Ref. 1).
 FT CONFLICT 115 115 S -> R (in Ref. 1).
 FT CONFLICT 211 211 T -> R (in Ref. 1).
 SQ SEQUENCE 473 AA; E504168191CB6429 CRC64;
 Query Match 96.6%; Score 2340.5; DB 1; Length 473;
 Best Local Similarity 96.6%; Pred. No. 2.1e-151;
 Matches 457; Conservative 6; Mismatches 9; Indels 1; Gaps 1;
 Qy 1 MKSILDLGLADTTTFTTTTLLYGSNDIQYEDIKGDMASKLGYFPQKPLTSFRGSPQE 60
 Db 1 MKSILDLGLADTTTFTTTTLLYGSNDIQYEDIKGDMASKLGYFPQKPLTSFRGSPQE 60
 Qy 61 KMTAGDNPOLVPA--DQVNTTFYKNSLSKKEENETOCGFENWDECFMVLNPSQQLAI 119
 Db 61 KMTAGDNPOLVPA--DQVNTTFYKNSLSKKEENETOCGFENWDECFMVLNPSQQLAI 120
 Qy 120 AVLSLTGLTFTVLENLVLCVILHSRLRCRPSYHFGSLAVADLGLSVIFVYSGFDPHV 179
 Db 121 AVLSLTGLTFTVLENLVLCVILHSRLRCRPSYHFGSLAVADLGLSVIFVYSGFDPHV 180
 Qy 180 FHRKDSRNVLFLKGGVTSAGTASVGLSFLTAIARYSIHRPLAYKRIIVTRPKAVAFCL 239
 Db 181 FHRKDSRNVLFLKGGVTSAGTASVGLSFLTAIARYSIHRPLAYKRIIVTRPKAVAFCL 240
 Qy 240 MWTIAIVAVLPILGNCKEQSCVDIPPHIDETVLMFVIGTSLVLLFVYVYVILW 299
 Db 241 MWTIAIVAVLPILGNCKEQSCVDIPPHIDETVLMFVIGTSLVLLFVYVYVILW 300
 Qy 300 KAHSHAVRMIOGRQTKSIIHTSBDGKQVTRPQARMARLAKTLVLILVVLICWGPL 359
 Db 301 KAHSHAVRMIOGRQTKSIIHTSBDGKQVTRPQARMARLAKTLVLILVVLICWGPL 360
 Qy 360 LAIMVYDVFGQNKLIKTVFAFCNMLCLLNSTVNPPIIYALRSKDLRHFRRMFPSCGTA 419
 Db 361 LAIMVYDVFGQNKLIKTVFAFCNMLCLLNSTVNPPIIYALRSKDLRHFRRMFPSCGTA 420
 Qy 420 QPLDNSMGDSCLHKHANNAASVHRAEASCISKSTVKIAKWTMSVSTDTSAAL 472
 Db 421 QPLDNSMGDSCLHKHANNAASVHRAEASCISKSTVKIAKWTMSVSTDTSAAL 473

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RESULT 9
Q5SF33 MOUSE
ID Q5SF33 MOUSE PRELIMINARY; PRT; 473 AA.
AC Q5SF33;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Striatal cannabinoid receptor type 1 protein.
GN Name=Cnr1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B6CBA;
RX PubMed=15606779; DOI=10.1111/j.1432-1033.2004.04460.x;
RA McCaw E.A., Hu H., Gomez G.T., Hebb A.L., Kelly M.E.,
RA Denovan-Wright E.M.;
RT "Structure, expression and regulation of the cannabinoid receptor gene
(CB1) in Huntington's disease transgenic mice.";
RL Eur. J. Biochem. 271:4909-4920(2004).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR EMBL; AY522555; AAS91801.1; -; Genomic_DNA.
DR EMBL; AY522554; AAS91800.1; -; mRNA.
DR MGI; MGI:104615; Cnr1.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR002230; Cnbnoid_receptor.
DR InterPro; IPR000810; Cnoid_receptor1.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00522; CANNABINOIDR.
DR PRINTS; PR00362; CANNABINOIDR.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR G-protein coupled receptor; Receptor; Transducer; Transmembrane.
KW SEQUENCE 473 AA; 52831 MW; E504168191CB6429 CRC64;

Query Match 96.6%; Score 2340.5; DB 2; Length 473;
Best Local Similarity 96.6%; Pred. No. 2.1e-151;
Matches 457; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

QY 1 MKSILDLADTTTPTTTTLLLYGSDNIQYEDIKGMASKLGYFPQKPLTSFRGSPFQE 60
DB 1 MKSILDLADTTTPTTTTLLLYGSDNIQYEDIKGMASKLGYFPQKPLTSFRGSPFQE 60

QY 61 KMTAGNPOLVPA-DQVNTTEFYNKSLSPKNEENIQCGENFMDIECFMVLNPSQQLAI 119
DB 61 KMTAGNPOLVPA-DQVNTTEFYNKSLSPKNEENIQCGENFMDIECFMVLNPSQQLAI 120

QY 120 AVLSLTGLFTVLENLVLCVILHSRLCRPSYHFIGSLAVADLLGSIYFVYSFIDFHV 179
DB 121 AVLSLTGLFTVLENLVLCVILHSRLCRPSYHFIGSLAVADLLGSIYFVYSFIDFHV 180

QY 180 FHRKDSRNPLFKLGGVTSFTASVGSFLTAJARIYSIHRPLAYKRIYTRPKAVVAFCL 239
DB 181 FHRKDSRNPLFKLGGVTSFTASVGSFLTAJARIYSIHRPLAYKRIYTRPKAVVAFCL 240

QY 240 MWTIAIVAVLPVLGNWCKLQSCVSDIPPHIDETVLMFWIGVTSVLLLFIVVAYVYILW 299
DB 241 MWTIAIVAVLPVLGNWCKLQSCVSDIPPLIDETVLMFWIGVTSVLLLFIVVAYVYILW 300

QY 300 KAHSHAVRMITQRTQKSIITHTSDGKQVQTRPDQARMAIRLAKTLVLVLIIICWGPL 359
DB 301 KAHSHAVRMITQRTQKSIITHTSDGKQVQTRPDQARMDIRLAKTLVLVLIIICWGPL 360

QY 360 LAIMVYDVFGKMKLKTVPFACSMCLLNSTVNPYIYALRSKDLRHAFRSPFSCGTA 419
DB 361 LAIMVYDVFGKMKLKTVPFACSMCLLNSTVNPYIYALRSKDLRHAFRSPFSCGTA 420
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QY 420 QPLDMSGDSCLHKKHANAASVHRAESCIKSTVKIAKVTMSVSTDTSAEAL 472
DB 421 QPLDMSGDSCLHKKHANAASVHRAESCIKSTVKIAKVTMSVSTDTSAEAL 473

RESULT 10
CNRL_FELCA
ID CNRL_FELCA STANDARD; PRT; 472 AA.
AC Q02777;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Cannabinoid receptor 1 (CB1) (CB-R).
GN Name=CNRL1;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC Felinae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gebremedhin D., Lange A.R., Aebly M.R., Campbell W.B., Hillard C.J.,
RA Harder D.R.;
RT "The cannabinoid CB1 receptor is expressed in cat cerebral arterial
muscle cells and functions to inhibit L-type Ca2+ channel current."
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Involved in cannabinoid-induced CNS effects. Acts by
inhibiting adenylylate cyclase. Could be a receptor for anandamide.
CC -!- Inhibits L-type Ca(2+) channel current.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in cerebral arterial muscle cells.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.

EMBL; U94342; AAS93440.1; -; mRNA.
InterPro; IPR002230; Cnbnoid_receptor.
InterPro; IPR000810; Cnoid_receptor1.
InterPro; IPR000276; GPCR_Rhodopsn.
PANTHER; PTHR19266:SP8; Cnoid_receptor1; 1.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00522; CANNABINOIDR.
PRINTS; PR00362; CANNABINOIDR.
PRINTS; PR00237; GPCR_RHODOPSIN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Glycoprotein; Receptor; Transducer;
Transmembrane.
TOPO_DOM 1 116 Extracellular (Potential).
TRANSMEM 117 142 1 (Potential).
TOPO_DOM 143 154 Cytoplasmic (Potential).
TRANSMEM 155 175 2 (Potential).
TOPO_DOM 176 187 Extracellular (Potential).
TRANSMEM 188 212 3 (Potential).
TOPO_DOM 213 232 Cytoplasmic (Potential).
TRANSMEM 233 255 4 (Potential).
TOPO_DOM 256 273 Extracellular (Potential).
TRANSMEM 274 299 5 (Potential).
TOPO_DOM 300 344 Cytoplasmic (Potential).
TRANSMEM 345 365 6 (Potential).
TOPO_DOM 366 377 Extracellular (Potential).
TRANSMEM 378 399 7 (Potential).
TOPO_DOM 400 472 Cytoplasmic (Potential).
CARBOHYD 77 77 N-linked (GlcNAc...) (Potential).
CARBOHYD 83 83 N-linked (GlcNAc...) (Potential).
SEQUENCE 472 AA; 52887 MW; A2774DBF8F2DAF34 CRC64;

Query Match 96.3%; Score 2335; DB 1; Length 472;
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Best Local Similarity 95.8%; Pred. No. 5e-151;		Matches 452; Conservative 13; Mismatches 7; Indels 0; Gaps 0;	
QY	1	MKSILDLGLADTTTTRTTTDLVYGSNDIQYEDIKGDMASKLGYFPQKFPPLTSFRGSPFQE	60
Db	1	MKSILDLGLADTTTTRTTTDLVYGSNDIQYEDIKGDMASKLGYFPQKFPPLTSFRGSPFQE	60
QY	61	KMTAGNPQLVPADQVNIITFYFNKSLSSFKENEENIQCGENFMDIECFMVLNPSQQLAIA	120
Db	61	KMTAGNSQLVPADQVNIITFYFNKSLSSYKENEENIQCGENFMDIECFMVLNPSQQLAIA	120
QY	121	VLSITLGTFTVLENLVLCVILHSRSLRCRPSYHFGISLAVADLLGSLVIFVYSFIDPHVF	180
Db	121	VLSITLGTFTVLENLVLCVILHSRSLRCRPSYHFGISLAVADLLGSLVIFVYSFIDPHVF	180
QY	181	HRKDSRNVFLFKGGVTASTASVGSFLTAIARYISIHRLAYKRIIVTRPKAVAFCLM	240
Db	181	HRKDSPNVFLFKGGVTASTASVGSFLTAIDRYISIHRLAYKRIIVTRPKAVAFCLM	240
QY	241	WTIAIVIAVPLLGWCKLQSCSDIFPHIDETYLMMFWIGVTSVLLLFIVAYMYILWK	300
Db	241	WTIAIVIAVPLLGWCKLQSCSDIFPLIDETYLMMFWIGVTSVLLLFIVAYMYILWK	300
QY	301	AHSHAVRMIOGTOKSIIHTSEDGKVQVTRPDQARMAIRLAKTLVLILVLIICWGPLL	360
Db	301	AHSHAVRMIOGTOKSIIHTSEDGKVQVTRPDQARMDIRLAKTLVLILVLIICWGPLL	360
QY	361	AIMYDVFGRKMKLIKTVAFCSMLCLLNSTVNPPIIYALRSKOLRHAFRSMFSPCECTAQ	420
Db	361	AIMYDVFGRKMKLIKTVAFCSMLCLLNSTVNPPIIYALRSKOLRHAFRSMFSPCECTAQ	420
QY	421	PLDSMGDSCLHGHANNAASVHRAAESCKSTVKIAKVTMSVSTDSAEAL	472
Db	421	PLDSMGDSCLHGHANNTANVHRAAENCKNTVQIAKVTISVSTNTSAKAL	472
RESULT 11			
CNRI	POEGU	STANDARD;	PRT; 473 AA.
ID	CNRI	POEGU	
AC	P56971;		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	13-SEP-2005 (Rel. 48, Last annotation update)		
DE	Cannabinoid receptor 1 (CBI) (CB-R).		
GN	Name=CNRI;		
OS	Poephila guttata (Zebra finch) (Taeniopygia guttata).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Archosauria; Aves; Neognathae; Passeriformes; Estrildidae;		
OC	Estrildinae; Taeniopygia.		
OX	NCBI_TaxID=59729;		
RN	(1)		
RP	NUCLEOTIDE SEQUENCE.		
RA	Soderstrom K., Johnson F.;		
RT	"Behavioral, pharmacologic and molecular characterization of a Zebra		
RT	finch CBI cannabinoid receptor.";		
RL	Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.		
CC	-1- FUNCTION: Involved in cannabinoid-induced CNS effects. Acts by		
CC	inhibiting adenylylate cyclase (By similarity).		
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.		
CC	-----		
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use as long as its content is in no way modified and this statement is not		
CC	removed.		
CC	-----		
DR	EMBL; AF255388; AAF78049.1; -; mRNA.		
DR	InterPro; IPR002230; Cnbnoid_receptor.		
DR	InterPro; IPR000810; Cnoid_receptor1.		
DR	InterPro; IPR000276; GPCR_Rhodopsin.		
DR	PANTHER; PTHR19286:SF8; Cnoid_receptor1; 1.		
DR	Pfam; PF00001; 7tm_1; 1.		

DR	PRINTS; PR00522;	CANABINOIDIR.	
DR	PRINTS; PR00362;	CANNABINOIDR.	
DR	PRINTS; PR00237;	GPCRHODOPSN.	
DR	PROSITE; PS00237;	G-PROTEIN_RECEP_F1_1; 1.	
DR	PROSITE; PS0262;	G-PROTEIN_RECEP_F1_2; 1.	
KW	G-protein coupled receptor; Glycoprotein; Receptor; Transducer; Transmembrane.		
FT	TOPO_DOM	1	118 Extracellular (Potential).
FT	TRANSMEM	119	1 (Potential).
FT	TOPO_DOM	145	156 Cytoplasmic (Potential).
FT	TRANSMEM	157	177 2 (Potential).
FT	TOPO_DOM	178	189 Extracellular (Potential).
FT	TRANSMEM	190	214 3 (Potential).
FT	TOPO_DOM	215	234 Cytoplasmic (Potential).
FT	TRANSMEM	235	257 4 (Potential).
FT	TOPO_DOM	258	275 Extracellular (Potential).
FT	TRANSMEM	276	301 5 (Potential).
FT	TOPO_DOM	302	346 Cytoplasmic (Potential).
FT	TRANSMEM	347	367 6 (Potential).
FT	TOPO_DOM	368	379 Extracellular (Potential).
FT	TRANSMEM	380	401 7 (Potential).
FT	TOPO_DOM	402	473 Cytoplasmic (Potential).
FT	CARBOHYD	79	79 N-linked (GlcNAc...) (Potential).
FT	CARBOHYD	85	85 N-linked (GlcNAc...) (Potential).
SQ	SEQUENCE	473 AA;	96EC6D1BD25461E CRC64;
Query Match 92.8%; Score 2250.5; DB 1; Length 473;			
Best Local Similarity 91.4%; Pred. No. 2.9e-145;			
Matches 433; Conservative 25; Mismatches 13; Indels 3; Gaps 2;			
QY	1	MKSILDLGLADTTTTRTTTDLVYGSNDIQYEDIKGDMASKLGYFPQKFPPLTSFRGSPFQE	60
Db	1	MKSILDLGLADTTTTRTTTDLVYGSNDIQYEDIKGDMASKLGYFPQKFPPLTSFRGSPFQE	60
QY	61	KMTAGNMP--QLVPADQVNIITFYFNKSLSSFKENEENIQCGENFMDIECFMVLNPSQQLA	118
Db	61	KMTGGDLSLSIIPSEQVNITEFYFNKSLSTFKONEENIQCGENFMDIECFMVLNPSQQLA	120
QY	119	IAVLSITLGTFTVLENLVLCVILHSRSLRCRPSYHFGISLAVADLLGSLVIFVYSFIDPH	178
Db	121	IAVLSITLGTFTVLENLVLCVILHSRSLRCRPSYHFGISLAVADLLGSLVIFVYSFIDPH	180
QY	179	VFHRKDSRNVFLFKGGVTASTASVGSFLTAIARYISIHRLAYKRIIVTRPKAVAFVC	238
Db	181	VFHRKDSPNVFLFKGGVTASTASVGSFLTAIDRYISIHRLAYKRIIVTRPKAVAFVC	240
QY	239	LMWTIAIVIAVPLLGWCKLQSCSDIFPHIDETYLMMFWIGVTSVLLLFIVAYMYIL	298
Db	241	VMTIAIVIAVPLLGWCKLQSCSDIFPLIDETYLMMFWIGVTSVLLLFIVAYMYIL	300
QY	299	WKAHSHAVRMIOGTOKSIIHTSEDGKVQVTRPDQARMAIRLAKTLVLILVLIICWGP	358
Db	301	WKAHSHAVRMIOGTOKSIIHTSEDGKVQVTRPDQARMDIRLAKTLVLILVLIICWGP	360
QY	359	LLAIAWYDVFGKMKLIKTVAFCSMLCLLNSTVNPPIIYALRSKOLRHAFRSMFSPCEGT	418
Db	361	LLAIAWYDVFGKMKLIKTVAFCSMLCLLNSTVNPPIIYALRSKOLRHAFRSMFSPCEGT	420
QY	419	AQPLDMSGDSCLHGHANNAASVHRAAESCKSTVKIAKVTMSVSTDSAEAL	472
Db	421	AQPLDMSGDSCLHGHANNTANVHRAAENCKNTVQIAKVTMSVSTDTTAAAL	473
RESULT 12			
Q5UB37	HUMAN		
ID	Q5UB37	HUMAN PRELIMINARY;	PRT; 439 AA.
AC	O5UB37;		
DT	01-FEB-2005 (TrEMBLrel. 29, Created)		
DT	01-FEB-2005 (TrEMBLrel. 29, Last sequence update)		
DT	01-FEB-2005 (TrEMBLrel. 29, Last annotation update)		
DE	Cannabinoid receptor 1 splice variant Cblb.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		

OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15620723; DOI=10.1016/j.febslet.2004.11.085;
 RA Ryberg E., Vu H.K., Larsson N., Groblewski T., Hjorth S., Elebring T.,
 RA Sjogren S., Greasley P.J.;
 RT "Identification and characterisation of a novel splice variant of the
 RT human Cbl receptor.";
 RL FEBS Lett. 579:259-264(2005).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Khang Vu H., Groblewski T., Greasley P.;
 RA Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 DR EMBL; AY766182; AAV3030.1; -; mRNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004949; F:cannabinoid receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR002230; Cnbnoid receptor.
 DR InterPro; IPR000810; Cnoid receptor1.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00522; CANABINOIDIR.
 DR PRINTS; PR00362; CANABINOIDIR.
 DR PRINTS; PR00237; GPCR_RHODOPSIN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
 SQ SEQUENCE 439 AA; 49060 MW; C80C6B8D640412C1 CRC64;
 Query Match 91.2%; Score 2209.5; DB 2; Length 439;
 Best Local Similarity 92.6%; Pred. No. 1.7e-142;
 Matches 437; Conservative 0; Mismatches 12; Indels 33; Gaps 1;
 QY 1 MXSILDLGLADTTFRITTTDLLVYGSNDIQYEDIKGDMASKLGYFPKFLTSFRGSPFQ 60
 DB 1 MXSILDLGLADTTFRITTTDLLVYGSNDIQYEDIKGDMASKLGYFPKFLTSFRGSPFQ 27
 QY 61 KMTAGNPNQLVPADQVNIETFYNKSLSFKENEENIQCGENFMDIECFMVLNPSQQLA 120
 DB 28 KMTAGNPNQLVPADQVNIETFYNKSLSFKENEENIQCGENFMDIECFMVLNPSQQLA 87
 QY 121 VLSLTGTFTVLENLVLCVILHSRLCRPSVHFPGSLAVADLLGSLVFVYSFIDFHFV 180
 DB 88 VLSLTGTFTVLENLVLCVILHSRLCRPSVHFPGSLAVADLLGSLVFVYSFIDFHFV 147
 QY 181 HRKDSRNVLFLKGGVYASTASVGSIFLTAIRYISIHRLAYKRIIVTRPKAVAFCLM 240
 DB 148 HRKDSRNVLFLKGGVYASTASVGSIFLTAIRYISIHRLAYKRIIVTRPKAVAFCLM 207
 QY 241 WTIAIVIAVLPLGWNCKLQSVCSDFPHIDETILMFVIGVTSVLLLFVYAYMILWK 300
 DB 208 WTIAIVIAVLPLGWNCKLQSVCSDFPHIDETILMFVIGVTSVLLLFVYAYMILWK 267
 QY 301 AHSNAVMTQRGQTKSIITHTSDGKQVTRPQARMAIRLAKTILVLVLIICWGPLL 360
 DB 268 AHSNAVMTQRGQTKSIITHTSDGKQVTRPQARMDIRLAKTILVLVLIICWGPLL 327
 QY 361 AIMVYDFGQWKLITKTVAFCSMLCLLNTVPIIYALRSKDLRHAFRSMRPPSCGTQA 420
 DB 328 AIMVYDFGQWKLITKTVAFCSMLCLLNTVPIIYALRSKDLRHAFRSMRPPSCGTQA 387
 QY 421 PLDNSMGDSCLLKHANNAASVHRAAESCIKSTVKIAKVTMSVTDTSAEAL 472
 DB 388 PLDNSMGDSCLLKHANNAASVHRAAESCIKSTVKIAKVTMSVTDTSAEAL 439
 RESULT 13

CNRI_TARGR
 ID CNRI_TARGR STANDARD; PRT; 473 AA.
 AC Q9PUI7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Cannabinoid receptor 1 (Cbl) (CB-R).
 GN Name=CNRI;
 OS Taricha granulosa (Roughskin newt).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Taricha.
 OX NCBI_TaxID=8321;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20312895; PubMed=10854287;
 RA Soderstrom K., Leid M., Moore F.L., Murray T.F.;
 RT "Behavioral, pharmacological, and molecular characterization of an
 RT amphibian cannabinoid receptor.";
 RL J. Neurochem. 75:413-423(2000).
 CC -1- FUNCTION: Involved in cannabinoid-induced CNS effects. Acts by
 CC -1- inhibiting adenylylate cyclase (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; AF181894; AAD56029.1; -; mRNA.
 DR InterPro; IPR002230; Cnbnoid receptor.
 DR InterPro; IPR000810; Cnoid receptor1.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR PANTHER; PTHR19266:SP8; Cnoid_receptor1; 1.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00522; CANABINOIDIR.
 DR PRINTS; PR00362; CANABINOIDIR.
 DR PRINTS; PR00237; GPCR_RHODOPSIN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Receptor; Transducer;
 KW Transmembrane.
 FT TOPO_DOM 1 118 Extracellular (Potential).
 FT TRANSMEM 119 144 1 (Potential).
 FT TOPO_DOM 145 156 Cytoplasmic (Potential).
 FT TRANSMEM 157 177 2 (Potential).
 FT TOPO_DOM 178 189 Extracellular (Potential).
 FT TRANSMEM 190 214 3 (Potential).
 FT TOPO_DOM 215 234 Cytoplasmic (Potential).
 FT TRANSMEM 235 257 4 (Potential).
 FT TOPO_DOM 258 275 Extracellular (Potential).
 FT TRANSMEM 276 301 5 (Potential).
 FT TOPO_DOM 302 346 Cytoplasmic (Potential).
 FT TRANSMEM 347 367 6 (Potential).
 FT TOPO_DOM 368 379 Extracellular (Potential).
 FT TRANSMEM 380 401 7 (Potential).
 FT TOPO_DOM 402 473 Cytoplasmic (Potential).
 FT CARBOHYD 79 79 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 85 85 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 473 AA; 53325 MW; F17C016516ED4724 CRC64;
 Query Match 85.2%; Score 2064.5; DB 1; Length 473;
 Best Local Similarity 83.5%; Pred. No. 1.4e-132;
 Matches 396; Conservative 39; Mismatches 36; Indels 3; Gaps 2;
 QY 1 MXSILDLGLADTTFRITTTDLLVYGSNDIQYEDIKGDMASKLGYFPKFLTSFRGSPFQ 60
 DB 1 MXSILDLGLADTTFRITTTDLLVYGSNDIQYEDIKGDMASKLGYFPKFLTSFRGSPFQ 60
 QY 61 KMTAGNPNQL--VPADQVNIETFYNKSLSFKENEENIQCGENFMDIECFMVLNPSQQLA 118
 DB 61 KMTIGDNNLLSFYPLDQFNVTFFNRSVSTFFKENDNKLKGENFMDIECFMILTASQQLI 120

QY 119 IAVLSLTGFTVLENLVLCVILHSRLCRPSYHFIGSLAVADLLGSIYFVYSFIDEH 178
DB 121 IAVLSLTGFTVLENLVLCVILHSRLCRPSYHFIGSLAVADLLGSIYFVYSFIDEH 180
QY 179 VFKRDSRNFLFKLGCVTASFTASVGSFLTAIARYISIHRLAYKRIIVTRPKAVAVFC 238
DB 181 VFKRDSRNFLFKLGCVTASFTASVGSFLTAIARYISIHRLAYKRIIVTRPKAVAVFC 240
QY 239 LMTIAIVAVPLLGWNCSEKLSVCSDDIPPHIDETVLMFWIGVTSVLLLFIVAYMYIL 298
DB 241 VMTIAIIIAVPLLGWNCSEKLSVCSDDIPPHIDETVLMFWIGVTSVLLLFIVAYMYIL 300
QY 299 WKASHAVRMVLRQGTOKSIIHTSDEGKVQVTRPDQARMAIRLAKTLVLLVLIICWGP 358
DB 301 WKASHAVRMVLRQGTOKSIIHTSDEGKVQVTRPDQARMAIRLAKTLVLLVLIICWGP 360
QY 359 LLAIMVYDVFQKMKLKTVPFACSMCLNLTNPPIIYALRSKDLRHAFRSPSCCEGT 418
DB 361 LLAIMVYDVFQKMKLKTVPFACSMCLNLTNPPIIYALRSKDLRHAFRSPSCCEGT 420
QY 419 AQLDNSMGSDCLHKKHANNAAHVRAAESCIKSTVKIAKVTMSVSTDSABAL 472
DB 421 SQLDNSM-ESDCQHRHGNAGVHRAAENCISKSTVKIAKVTMSVSTDSABAL 473

RESULT 14
Q801M1 XENLA PRELIMINARY; PRT; 470 AA.
AC Q801M1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CBI cannabinoid receptor.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP MEDLINE=22782291; PubMed=12297261; DOI=10.1016/S0891-0618(02)00040-6;
RX Salio C., Cottone E., Conrath M., Franzoni M.F.;
RA "Cbi cannabinoid receptors in amphibian spinal cord: relationships
RT with some nociception markers.";
RN J. Chem. Neuroanat. 24:153-162(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22782291; PubMed=12297261; DOI=10.1002/cne.10808;
RA Cottone E., Salio C., Conrath M., Franzoni M.F.;
RT "Xenopus laevis CBI cannabinoid receptor: molecular cloning and mRNA
RN distribution in the central nervous system.";
RN J. Comp. Neurol. 464:487-496(2003).
RN [3]
RP NUCLEOTIDE SEQUENCE.

RA Cottone E.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR EMBL; AY098532; AAM28314.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004949; F:cannabinoid receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR002230; Cnbnoid_receptor.
DR InterPro; IPR000810; Cnoid_receptor1.
DR InterPro; IPR002276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00522; CANNABINOIDR.
DR PRINTS; PR00362; CANNABINOIDR.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_FL1_2; 1.

KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 470 AA; 52778 MW; 388EA7881064C950 CRC64;
Query Match 83.8%; Score 2031; DB 2; Length 470;
Best Local Similarity 82.7%; Pred. No. 2.7e-130;
Matches 391; Conservative 43; Mismatches 35; Indels 4; Gaps 4;
QY 1 MKSILDLGLADTTTFTTTTLLVYSGNDIQYEDIKGMASKLGYFPQKFPPTTSFRGSPQE 60
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DB 61 KMTIIDDPLSLIPDQINATDFYKSI-IFKDTDDNVQCGKNFMDMECFMLTSPQQLVI 119
QY 120 AVLSLTGTFTVLENLVLCVILHSRLCRPSYHFIGSLAVADLLGSIYFVYSFIDEH 179
DB 120 AALSIIIGTFTVLENLVLCVILHSRLCRPSYHFIGSLAVADLLGSIYFVYSFIDEH 179
QY 180 FHRKDSRNFLFKLGCVTASFTASVGSFLTAIARYISIHRLAYKRIIVTRPKAVAVFC 239
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DB 240 MWTIAIVAVPLLGWNCSEKLSVCSDDIPPHIDETVLMFWIGVTSVLLLFIVAYMYIL 299
QY 300 KASHAVRMVLRQGTOKSIIHTSDEGKVQVTRPDQARMAIRLAKTLVLLVLIICWGP 359
DB 300 KASHAVRMVLRQGTOKSIIHTSDEGKVQVTRPDQARMAIRLAKTLVLLVLIICWGP 359
QY 360 LAIMVYDVFQKMKLKTVPFACSMCLNLTNPPIIYALRSKDLRHAFRSPSCCEGT 419
DB 360 LAIMVYDVFQKMKLKTVPFACSMCLNLTNPPIIYALRSKDLRHAFRSPSCCEGT 419
QY 420 QPLDNSMGSDCLHKKHANNAAHVRAAESCIKSTVKIAKVTMSVSTDSABAL 472
DB 420 QPLDNSM-ESDCQHRHGNAGVHRAAENCISKSTVKIAKVTMSVSTDSABAL 470

RESULT 15

Q5JVL5 HUMAN PRELIMINARY; PRT; 411 AA.
AC Q5JVL5;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE OTTHUMP00000016840.
GN Name=CNRI; ORFNames=RP1-23D17.1-003;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Williams S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR EMBL; AL136096; CA119916.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004949; F:cannabinoid receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR002230; Cnbnoid_receptor.
DR InterPro; IPR000810; Cnoid_receptor1.
DR InterPro; IPR002276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00522; CANNABINOIDR.
DR PRINTS; PR00362; CANNABINOIDR.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_FL1_2; 1.

KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 411 AA; 45874 MW; E3C31ACAB4066BC1 CRC64;

Query Match		80.6%;	Score 1954;	DB 2;	Length 411;
Best Local Similarity		98.5%;	Pred. No. 4.1e-125;		
Matches 382;		Conservative 1;	Mismatches 5;	Indels 0;	Gaps 0;
QY	85	SISSPFKENBENIOCGNFMDIECFMVLNPSQQIAIAVLSITLGTFTVLENLLVLCVILHS	144		
Db	24	SIKTSKENBENIOCGNFMDIECFMVLNPSQQIAIAVLSITLGTFTVLENLLVLCVILHS	83		
QY	145	RSILRCRPSYHFIGSLAVADLLGSVIFVYSFIDPHVPHRKDSRNVFLFKLGGVTASTASV	204		
Db	84	RSILRCRPSYHFIGSLAVADLLGSVIFVYSFIDPHVPHRKDSRNVFLFKLGGVTASTASV	143		
QY	205	GSILFLTAIARYISIHRLAYKRIIVTRPKAVAFCLMWTIAIVAVLPILGWNCEKLOSVC	264		
Db	144	GSILFLTAIDRYISIHRLAYKRIIVTRPKAVAFCLMWTIAIVAVLPILGWNCEKLOSVC	203		
QY	265	SDIFFPHIDETFLMFWIGVTSVLLLFIVYAYMYILWKASHAVRMIOQTQKSIIIHTSED	324		
Db	204	SDIFFPHIDETFLMFWIGVTSVLLLFIVYAYMYILWKASHAVRMIOQTQKSIIIHTSED	263		
QY	325	GKQVTRPDQARMIAIRLAKTLVLILVLIICWGPELLAIMVYDVFGKGNKLIKTVFAPCSM	384		
Db	264	GKQVTRPDQARMIRLAKTLVLILVLIICWGPELLAIMVYDVFGKGNKLIKTVFAPCSM	323		
QY	385	LCILNSTVNPPIIYALRSKDLRHAFRSMFPSCGTAQPLDNSMGDSDCILHKHANNAAVHR	444		
Db	324	LCILNSTVNPPIIYALRSKDLRHAFRSMFPSCGTAQPLDNSMGDSDCILHKHANNAAVHR	383		
QY	445	AAESCICKSTVKIAKVTMSVSTDTSAEAL	472		
Db	384	AAESCICKSTVKIAKVTMSVSTDTSAEAL	411		

Search completed: January 6, 2006, 21:12:26
Job time : 235 secs

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OM protein - protein search, using sw model

Run on: January 6, 2006, 21:05:18 ; Search time 167 seconds
(without alignments)

1180.931 Million cell updates/sec

Title: US-10-521-420-1

Perfect score: 2424

Sequence: 1 MKSILDGLADTTTFTTTDL.....TVKIAKVTMSVSTDSAEAL 472

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2424	100.0	472	5	US-10-521-420-1
2	2412	99.5	472	4	US-10-225-567A-84
3	2412	99.5	472	4	US-10-029-386-33685
4	2412	99.5	472	4	US-10-295-027-236
5	2412	99.5	472	4	US-10-764-425-168
6	2412	99.5	472	5	US-10-482-029-172
7	2412	99.5	472	3	US-11-019-829-88
8	2407	99.3	472	3	US-09-826-509-469
9	2407	99.3	472	5	US-10-925-095-469
10	2401	99.1	472	4	US-10-295-027-238
11	1954	80.6	411	4	US-10-295-027-240
12	1954	80.6	411	4	US-10-408-765A-2310
13	1954	80.6	411	6	US-11-019-829-89
14	710	29.3	360	4	US-10-225-567A-86
15	710	29.3	360	4	US-10-290-078-3
16	710	29.3	360	5	US-10-473-127-1541
17	710	29.3	360	5	US-10-473-127-1542
18	710	29.3	360	5	US-10-473-127-1543
19	710	29.3	360	5	US-10-473-127-1544
20	705	29.1	360	3	US-09-826-509-471
21	705	29.1	360	5	US-10-925-095-471
22	410	16.9	80	3	US-09-993-844-50
23	410	16.9	80	4	US-10-633-438-36
24	410	16.9	80	5	US-10-693-164-38
25	410	16.9	80	5	US-10-901-772-36
26	410	16.9	80	6	US-11-026-435-50
27	369.5	15.2	362	3	US-09-993-844-8

28	369.5	15.2	362	4	US-10-633-438-65	Sequence 65, Appl
29	369.5	15.2	362	5	US-10-901-772-65	Sequence 65, Appl
30	369.5	15.2	362	6	US-11-026-435-8	Sequence 8, Appl
31	366	15.1	391	3	US-09-904-099-3	Sequence 3, Appl
32	364.5	15.0	384	3	US-09-904-099-4	Sequence 4, Appl
33	364	15.0	364	3	US-09-904-099-30	Sequence 30, Appl
34	364	15.0	364	4	US-10-228-762-15	Sequence 15, Appl
35	364	15.0	364	4	US-10-648-593-166	Sequence 166, App
36	364	15.0	364	4	US-10-764-425-130	Sequence 130, App
37	364	15.0	364	4	US-10-741-601-489	Sequence 489, App
38	364	15.0	364	4	US-10-741-601-490	Sequence 490, App
39	364	15.0	364	4	US-10-741-601-491	Sequence 491, App
40	364	15.0	364	4	US-10-741-601-492	Sequence 492, App
41	364	15.0	364	4	US-10-741-601-493	Sequence 493, App
42	364	15.0	364	5	US-10-741-600-1409	Sequence 1409, Ap
43	364	15.0	364	5	US-10-741-600-1410	Sequence 1410, Ap
44	364	15.0	364	5	US-10-741-600-1411	Sequence 1411, Ap
45	364	15.0	364	5	US-10-741-600-1412	Sequence 1412, Ap

ALIGNMENTS

RESULT 1

US-10-521-420-1

; Sequence 1, Application US/10521420

; Publication No. US20050239133A1

; GENERAL INFORMATION:

; APPLICANT: Greasley, Peter

; TITLE OF INVENTION: Methods to Identify True Antagonists and Inverse Agonists of the

; FILE REFERENCE: ASZD-P01-752

; CURRENT APPLICATION NUMBER: US/10/521,420

; CURRENT FILING DATE: 2005-01-14

; PRIOR APPLICATION NUMBER: SE 0202242-4

; PRIOR FILING DATE: 2002-07-17

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 472

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-521-420-1

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Matches 472;	Conservative	0;		Gaps 0;
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RESULT 2

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US-10-225-567A-84
; Sequence 84, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-84
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Query Match 99.5%; Score 2412; DB 4; Length 472;
Best Local Similarity 99.6%; Pred. No. 6.8e-214;
Matches 470; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 121 VLSLTGTFVLENLVLCVILHSRLRCRPSYHFHIGSLAVADLLGSLVFVYSFIDFHFV 180
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RESULT 3

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US-10-029-386-33685
; Sequence 33685, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
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; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 33685
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL136096.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.22
; OTHER INFORMATION: SWISSPROT HIT: P21554, EVALUAE 0.00e+00
US-10-029-386-33685
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Query Match 99.5%; Score 2412; DB 4; Length 472;
Best Local Similarity 99.6%; Pred. No. 6.8e-214;
Matches 470; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 MKSILDGLADTTFRITITDLLLVGSDIQYEDIKGMASKLGYFPQKFLTSFRGSPFOE 60
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RESULT 4

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US-10-295-027-236
; Sequence 236, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
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;; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
;; FILE REFERENCE: 018501-012500US
;; CURRENT APPLICATION NUMBER: US/10/295,027
;; CURRENT FILING DATE: 2002-11-13
;; PRIOR APPLICATION NUMBER: US 09/663,733
;; PRIOR FILING DATE: 2000-09-15
;; PRIOR APPLICATION NUMBER: US 60/350,666
;; PRIOR FILING DATE: 2001-11-13
;; PRIOR APPLICATION NUMBER: US 60/335,394
;; PRIOR FILING DATE: 2001-11-15
;; PRIOR APPLICATION NUMBER: US 60/332,464
;; PRIOR FILING DATE: 2001-11-21
;; PRIOR APPLICATION NUMBER: US 60/334,393
;; PRIOR FILING DATE: 2001-11-29
;; PRIOR APPLICATION NUMBER: US 60/340,376
;; PRIOR FILING DATE: 2001-12-14
;; PRIOR APPLICATION NUMBER: US 60/347,211
;; PRIOR FILING DATE: 2002-01-08
;; PRIOR APPLICATION NUMBER: US 60/347,349
;; PRIOR FILING DATE: 2002-01-10
;; PRIOR APPLICATION NUMBER: US 60/355,250
;; PRIOR FILING DATE: 2002-02-08
;; PRIOR APPLICATION NUMBER: US 60/356,714
;; PRIOR FILING DATE: 2002-02-13
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 1386
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 236
;; LENGTH: 472
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-295-027-236

Query Match 99.5%; Score 2412; DB 4; Length 472;
Best Local Similarity 99.6%; Pred. No. 6.8e-214;
Matches 470; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 121 VLSLTGTFVLENLVLCVILHSRSLRCRPSYHFIGSLAVADLLGSVIFYYSFIDFHFV 180

Qy 181 HRKDSRNVPFLKLGGVTSFTASVGSLSFTAIARYISIHRLAYKRIVTRPKAVVAFCLM 240
Db 181 HRKDSRNVPFLKLGGVTSFTASVGSLSFTAIARYISIHRLAYKRIVTRPKAVVAFCLM 240

Qy 241 WTIAIVAVLPLLGWNCCKLQSVCSDFPHIDETVLMFWIGVTSVLLLFIVYAYMYILWK 300
Db 241 WTIAIVAVLPLLGWNCCKLQSVCSDFPHIDETVLMFWIGVTSVLLLFIVYAYMYILWK 300

Qy 301 AHSHAVRMIQRGTQKSIITHTSEDKVQVTRPDQARMAIRLAKTLVLVLVLLIICWGPPL 360
Db 301 AHSHAVRMIQRGTQKSIITHTSEDKVQVTRPDQARMAIRLAKTLVLVLVLLIICWGPPL 360

Qy 361 AIMVYDVFQKMKLIKTVAFPCSMCLLNSTVNPPIIYALRSKDLRHAFRSPFCEGTAQ 420
Db 361 AIMVYDVFQKMKLIKTVAFPCSMCLLNSTVNPPIIYALRSKDLRHAFRSPFCEGTAQ 420

Qy 421 PLDSMGSDCLHGHANNAASVHRAESCIKSTVKIAKVTMSVSTDTSAEAL 472
Db 421 PLDSMGSDCLHGHANNAASVHRAESCIKSTVKIAKVTMSVSTDTSAEAL 472

RESULT 5
US-10-764-425-168
; Sequence 168, Application US/10764425

;; Publication No. US20040146921A1
;; GENERAL INFORMATION:
;; APPLICANT: Bayer Pharmaceuticals Corporation
;; APPLICANT: Eveleigh, Deepa
;; APPLICANT: Bigwood, Douglas
;; APPLICANT: Taylor, Ian
;; TITLE OF INVENTION: EXPRESSION PROFILES FOR COLON CANCER AND METHODS OF USE
;; FILE REFERENCE: 5151
;; CURRENT APPLICATION NUMBER: US/10/764,425
;; CURRENT FILING DATE: 2004-01-23
;; PRIOR APPLICATION NUMBER: 60/442,582
;; PRIOR FILING DATE: 2003-01-24
;; NUMBER OF SEQ ID NOS: 191
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 168
;; LENGTH: 472
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-764-425-168

Query Match 99.5%; Score 2412; DB 4; Length 472;
Best Local Similarity 99.6%; Pred. No. 6.8e-214;
Matches 470; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MKSILDLGADTTFTTTTDLVYGSNDIQYEDIKGDWASKLGYFPQKFPPLTSFRGSPFQE 60
Db 1 MKSILDLGADTTFTTTTDLVYGSNDIQYEDIKGDWASKLGYFPQKFPPLTSFRGSPFQE 60

Qy 61 KMTAGDNPQLVPADQVNITEFYKNSLSFKENEENIOCGENFMDIECFWLNPSQOLAIA 120
Db 61 KMTAGDNPQLVPADQVNITEFYKNSLSFKENEENIOCGENFMDIECFWLNPSQOLAIA 120

Qy 121 VLSLTGTFVLENLVLCVILHSRSLRCRPSYHFIGSLAVADLLGSVIFYYSFIDFHFV 180
Db 121 VLSLTGTFVLENLVLCVILHSRSLRCRPSYHFIGSLAVADLLGSVIFYYSFIDFHFV 180

Qy 181 HRKDSRNVPFLKLGGVTSFTASVGSLSFTAIARYISIHRLAYKRIVTRPKAVVAFCLM 240
Db 181 HRKDSRNVPFLKLGGVTSFTASVGSLSFTAIARYISIHRLAYKRIVTRPKAVVAFCLM 240

Qy 241 WTIAIVAVLPLLGWNCCKLQSVCSDFPHIDETVLMFWIGVTSVLLLFIVYAYMYILWK 300
Db 241 WTIAIVAVLPLLGWNCCKLQSVCSDFPHIDETVLMFWIGVTSVLLLFIVYAYMYILWK 300

Qy 301 AHSHAVRMIQRGTQKSIITHTSEDKVQVTRPDQARMAIRLAKTLVLVLVLLIICWGPPL 360
Db 301 AHSHAVRMIQRGTQKSIITHTSEDKVQVTRPDQARMAIRLAKTLVLVLVLLIICWGPPL 360

Qy 361 AIMVYDVFQKMKLIKTVAFPCSMCLLNSTVNPPIIYALRSKDLRHAFRSPFCEGTAQ 420
Db 361 AIMVYDVFQKMKLIKTVAFPCSMCLLNSTVNPPIIYALRSKDLRHAFRSPFCEGTAQ 420

Qy 421 PLDSMGSDCLHGHANNAASVHRAESCIKSTVKIAKVTMSVSTDTSAEAL 472
Db 421 PLDSMGSDCLHGHANNAASVHRAESCIKSTVKIAKVTMSVSTDTSAEAL 472

RESULT 6
US-10-482-029-172
; Sequence 172, Application US/10482029
; Publication No. US20050037445A1
;; GENERAL INFORMATION:
;; APPLICANT: ODIN medical A/S
;; TITLE OF INVENTION: Oncology drug innovation
;; FILE REFERENCE: P 573 PC00
;; CURRENT APPLICATION NUMBER: US/10/482,029
;; CURRENT FILING DATE: 2003-12-29
;; NUMBER OF SEQ ID NOS: 437
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 172
;; LENGTH: 472
;; TYPE: PRT
;; ORGANISM: Homo sapiens

US-10-482-029-172

Query Match 99.5%; Score 2412; DB 5; Length 472;
Best Local Similarity 99.8%; Pred. No. 6.8e-214;
Matches 470; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKSILDGLADTTTTRITTTDLLYYGSDIOYEDIKGDMASKLGYFPQKPLTSFRGSPFQ 60
DB 1 MKSILDGLADTTTTRITTTDLLYYGSDIOYEDIKGDMASKLGYFPQKPLTSFRGSPFQ 60
QY 61 KMTAGNPOLVPADQVNITEFYFNKSLSSPKENEENIQCGENFMDIECFWVLPNSQOLAIA 120
DB 61 KMTAGNPOLVPADQVNITEFYFNKSLSSPKENEENIQCGENFMDIECFWVLPNSQOLAIA 120
QY 121 VLSLTGTFTVLENLLVLCVILHSRSLRCRPSYHFHFGSLAVADLLGSLVFVYSFIDFHFV 180
DB 121 VLSLTGTFTVLENLLVLCVILHSRSLRCRPSYHFHFGSLAVADLLGSLVFVYSFIDFHFV 180
QY 181 HRKDSRNVLFLKGGVTASFTASVGSFLTAIARYISIHRLPLAYKRIIVTRPKAVAFCLM 240
DB 181 HRKDSRNVLFLKGGVTASFTASVGSFLTAIARYISIHRLPLAYKRIIVTRPKAVAFCLM 240
QY 241 WTIAIVIAVPLLGWNCCKLQSVCSDFPHIDETVLMFWIGVTSVLLLFIVVAYMYILWK 300
DB 241 WTIAIVIAVPLLGWNCCKLQSVCSDFPHIDETVLMFWIGVTSVLLLFIVVAYMYILWK 300
QY 301 AHSHAVRMITQRGTQKSIITHTSDEGKVQVTRPDQARMAIRLAKTLVLILVLLIICWGPLL 360
DB 301 AHSHAVRMITQRGTQKSIITHTSDEGKVQVTRPDQARMAIRLAKTLVLILVLLIICWGPLL 360
QY 361 AIWVDVFGKMKLIKTVPFACSMCLLNSTVNPPIIYALRSKDLRHAFRSMPPSCBGTQA 420
DB 361 AIWVDVFGKMKLIKTVPFACSMCLLNSTVNPPIIYALRSKDLRHAFRSMPPSCBGTQA 420
QY 421 PLDNSMGSDCLHKHANNAAASHVRAAESCIKSTVKIAKVTMSVSTDTSAEAL 472
DB 421 PLDNSMGSDCLHKHANNAAASHVRAAESCIKSTVKIAKVTMSVSTDTSAEAL 472
RESULT 7
US-11-019-829-88
; Sequence 88, Application US/11019829
; Publication No. US20050136465A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann-La Roche Inc.
; TITLE OF INVENTION: Novel targets for obesity from subcutaneous fat
; FILE REFERENCE: 22304
; CURRENT APPLICATION NUMBER: US/11/019,829
; CURRENT FILING DATE: 2004-12-22
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 88
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: cannabinoid receptor 1 (brain) variant 1
; LOCATION: (1)..(472)
; OTHER INFORMATION: LocusID: 1268; NM_016083
US-11-019-829-88

Query Match 99.5%; Score 2412; DB 6; Length 472;
Best Local Similarity 99.8%; Pred. No. 6.8e-214;
Matches 470; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKSILDGLADTTTTRITTTDLLYYGSDIOYEDIKGDMASKLGYFPQKPLTSFRGSPFQ 60
DB 1 MKSILDGLADTTTTRITTTDLLYYGSDIOYEDIKGDMASKLGYFPQKPLTSFRGSPFQ 60
QY 61 KMTAGNPOLVPADQVNITEFYFNKSLSSPKENEENIQCGENFMDIECFWVLPNSQOLAIA 120
DB 61 KMTAGNPOLVPADQVNITEFYFNKSLSSPKENEENIQCGENFMDIECFWVLPNSQOLAIA 120

QY 121 VLSLTGTFTVLENLLVLCVILHSRSLRCRPSYHFHFGSLAVADLLGSLVFVYSFIDFHFV 180
DB 121 VLSLTGTFTVLENLLVLCVILHSRSLRCRPSYHFHFGSLAVADLLGSLVFVYSFIDFHFV 180
QY 181 HRKDSRNVLFLKGGVTASFTASVGSFLTAIARYISIHRLPLAYKRIIVTRPKAVAFCLM 240
DB 181 HRKDSRNVLFLKGGVTASFTASVGSFLTAIARYISIHRLPLAYKRIIVTRPKAVAFCLM 240
QY 241 WTIAIVIAVPLLGWNCCKLQSVCSDFPHIDETVLMFWIGVTSVLLLFIVVAYMYILWK 300
DB 241 WTIAIVIAVPLLGWNCCKLQSVCSDFPHIDETVLMFWIGVTSVLLLFIVVAYMYILWK 300
QY 301 AHSHAVRMITQRGTQKSIITHTSDEGKVQVTRPDQARMAIRLAKTLVLILVLLIICWGPLL 360
DB 301 AHSHAVRMITQRGTQKSIITHTSDEGKVQVTRPDQARMAIRLAKTLVLILVLLIICWGPLL 360
QY 361 AIWVDVFGKMKLIKTVPFACSMCLLNSTVNPPIIYALRSKDLRHAFRSMPPSCBGTQA 420
DB 361 AIWVDVFGKMKLIKTVPFACSMCLLNSTVNPPIIYALRSKDLRHAFRSMPPSCBGTQA 420
QY 421 PLDNSMGSDCLHKHANNAAASHVRAAESCIKSTVKIAKVTMSVSTDTSAEAL 472
DB 421 PLDNSMGSDCLHKHANNAAASHVRAAESCIKSTVKIAKVTMSVSTDTSAEAL 472

RESULT 8
US-09-826-509-469
; Sequence 469, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, J-Lin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: Protein-Coupled Receptors
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 469
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-469

Query Match 99.3%; Score 2407; DB 3; Length 472;
Best Local Similarity 99.4%; Pred. No. 2e-213;
Matches 469; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKSILDGLADTTTTRITTTDLLYYGSDIOYEDIKGDMASKLGYFPQKPLTSFRGSPFQ 60
DB 1 MKSILDGLADTTTTRITTTDLLYYGSDIOYEDIKGDMASKLGYFPQKPLTSFRGSPFQ 60
QY 61 KMTAGNPOLVPADQVNITEFYFNKSLSSPKENEENIQCGENFMDIECFWVLPNSQOLAIA 120
DB 61 KMTAGNPOLVPADQVNITEFYFNKSLSSPKENEENIQCGENFMDIECFWVLPNSQOLAIA 120
QY 121 VLSLTGTFTVLENLLVLCVILHSRSLRCRPSYHFHFGSLAVADLLGSLVFVYSFIDFHFV 180
DB 121 VLSLTGTFTVLENLLVLCVILHSRSLRCRPSYHFHFGSLAVADLLGSLVFVYSFIDFHFV 180
QY 181 HRKDSRNVLFLKGGVTASFTASVGSFLTAIARYISIHRLPLAYKRIIVTRPKAVAFCLM 240
DB 181 HRKDSRNVLFLKGGVTASFTASVGSFLTAIARYISIHRLPLAYKRIIVTRPKAVAFCLM 240
QY 241 WTIAIVIAVPLLGWNCCKLQSVCSDFPHIDETVLMFWIGVTSVLLLFIVVAYMYILWK 300
DB 241 WTIAIVIAVPLLGWNCCKLQSVCSDFPHIDETVLMFWIGVTSVLLLFIVVAYMYILWK 300

301 AHSVAVMIQRTGKSIITHTSEDKVQVTRPDQARMAIRLAKTLVLVLVLIICWGPLL 360
301 AHSVAVMIQRTGKSIITHTSEDKVQVTRPDQARMDIRLKTTLVLVLVLIICWGPLL 360
361 AIMVYDVFGKMKLIKTVAFCSMLCLLNSTVNPPIIYALRSKDLRHAFRSMFPSCGTAQ 420
361 AIMVYDVFGKMKLIKTVAFCSMLCLLNSTVNPPIIYALRSKDLRHAFRSMFPSCGTAQ 420
421 PLDSMGSDCLHLKHANNAASVHRAAESCKSTVKIAKVTMSVSTDTSAEAL 472
421 PLDSMGSDCLHLKHANNAASVHRAAESCKSTVKIAKVTMSVSTDTSAEAL 472

RESULT 9
US-10-925-095-469
; Sequence 469, Application US/10925095
; Publication No. US20050019840A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/10/925,095
; CURRENT FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: US/09/826,509
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 469
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-925-095-469

Query Match 99.3%; Score 2407; DB 5; Length 472;
Best Local Similarity 99.4%; Pred. No. 2e-213;
Matches 469; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

421 1 MKSILDGLADTTFTTTTDLVYGSNDIQYEDIKGDMASKLGYFPQKPLTSFRGSPQ 60
421 1 MKSILDGLADTTFTTTTDLVYGSNDIQYEDIKGDMASKLGYFPQKPLTSFRGSPQ 60
61 KMTAGDNPOLVADQVNITEFYNKSLSFKNEENIQCGENFMDIECFVNLNPSQOLAIA 120
61 KMTAGDNPOLVADQVNITEFYNKSLSFKNEENIQCGENFMDIECFVNLNPSQOLAIA 120
121 VLSLTGTFVLENLVLCVILHRSRLCRPSYHFIGSLAVADLLGSVIFYSFIDFHFV 180
121 VLSLTGTFVLENLVLCVILHRSRLCRPSYHFIGSLAVADLLGSVIFYSFIDFHFV 180
181 HRKDSRNVPFLKGGVTASFTASVGSLSFLTAIRYISIHRLPLAYKRIIVTRPKAVVAFCLM 240
181 HRKDSRNVPFLKGGVTASFTASVGSLSFLTAIRYISIHRLPLAYKRIIVTRPKAVVAFCLM 240
241 WTIAIVIAVPLPLGWNCEKLSQVCSDDIPPHIDETVLMFWIGVTSVLLPIVYAVMYILWK 300
241 WTIAIVIAVPLPLGWNCEKLSQVCSDDIPPHIDETVLMFWIGVTSVLLPIVYAVMYILWK 300
301 AHSVAVMIQRTGKSIITHTSEDKVQVTRPDQARMAIRLAKTLVLVLVLIICWGPLL 360
301 AHSVAVMIQRTGKSIITHTSEDKVQVTRPDQARMDIRLKTTLVLVLVLIICWGPLL 360
361 AIMVYDVFGKMKLIKTVAFCSMLCLLNSTVNPPIIYALRSKDLRHAFRSMFPSCGTAQ 420
361 AIMVYDVFGKMKLIKTVAFCSMLCLLNSTVNPPIIYALRSKDLRHAFRSMFPSCGTAQ 420

421 PLDSMGSDCLHLKHANNAASVHRAAESCKSTVKIAKVTMSVSTDTSAEAL 472
421 PLDSMGSDCLHLKHANNAASVHRAAESCKSTVKIAKVTMSVSTDTSAEAL 472

RESULT 10
US-10-295-027-238
; Sequence 238, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 238
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-238

Query Match 99.1%; Score 2401; DB 4; Length 472;
Best Local Similarity 98.9%; Pred. No. 7.1e-213;
Matches 467; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

1 MKSILDGLADTTFTTTTDLVYGSNDIQYEDIKGDMASKLGYFPQKPLTSFRGSPQ 60
1 MKSILDGLADTTFTTTTDLVYGSNDIQYEDIKGDMASKLGYFPQKPLTSFRGSPQ 60
61 KMTAGDNPOLVADQVNITEFYNKSLSFKNEENIQCGENFMDIECFVNLNPSQOLAIA 120
61 KMTAGDNPOLVADQVNITEFYNKSLSFKNEENIQCGENFMDIECFVNLNPSQOLAIA 120
121 VLSLTGTFVLENLVLCVILHRSRLCRPSYHFIGSLAVADLLGSVIFYSFIDFHFV 180
121 VLSLTGTFVLENLVLCVILHRSRLCRPSYHFIGSLAVADLLGSVIFYSFIDFHFV 180
181 HRKDSRNVPFLKGGVTASFTASVGSLSFLTAIRYISIHRLPLAYKRIIVTRPKAVVAFCLM 240
181 HRKDSRNVPFLKGGVTASFTASVGSLSFLTAIRYISIHRLPLAYKRIIVTRPKAVVAFCLM 240

QY	138	LCVILHSRSLRCRPSYHFIGSLAVADLIGSVIFVYSFIDFHVHFKDSRNVFLFKLGGVT	197
Db	55	LYLILSSHQURRKPSYLFIGSLAGADFLASVFPACSFVNFHVHFGVDSKAVFLKIGSVT	114
QY	198	ASFTASVGSFLFLTAIARYISIIHRPLAYKRIVTRPKAVAFCLMWTIAIVIAVPLPLGMNC	257
Db	115	MTFTASVGSLLLTAIDRYLCRLYPSPSYKALLTRGRALVTLGIMWVLSALVSVPLPLMGWTC	174
QY	258	EKLQSVCSDFPFHIDETYLMPWIGVTSVLLLFIVYAYMYILWKAHSHAVRMIQRTOKSI	317
Db	175	--CPRECSLFPILIPNDYLLSWLLFIAFLFSGIITYTGHVLMKAHQHVA-----SL	223
QY	318	IIHTSEDKGVQVTRPDQARMA--IRLAKTILVLVLIIICWGPLLAIWVVDVFGKMKLI	375
Db	224	SGH--QDRQV----PGMARMLDVRLAKTILGLVLAVLLICWFPVLALMAHSLATILSDQV	277
QY	376	KTVFAFCSMCLLNSTVNPFIYALRSKDLR	405
Db	278	KKAFACSMCLCLNSMWNVPVIYALRSGEIR	307

Search completed: January 6, 2006, 21:16:59
Job time : 173 secs

Db	1	MKSILDGLADTTTTRTTITDLYYGSNDIQYEDIKGDMAKGLGYFPQKFLTSPRGSPFOE	60
QY	61	KMTAGNPOLVPADQVNIITFYNKLSLSPKENEENIQCGENFNDIECFWVLPNSQQALAI	120
Db	61	KMTAGNPOLVPADQVNIITFYNKLSLSPKENEENIQCGENFNDIECFWVLPNSQQALAI	120
QY	121	VLSLTGTFTVLENLLVLCVILHSRLCRPSYHFTIGSLAVADLLGSVIFVYSFIDFHFV	180
Db	121	VLSLTGTFTVLENLLVLCVILHSRLCRPSYHFTIGSLAVADLLGSVIFVYSFIDFHFV	180
QY	181	HRKDSRNVLFLKGGVTASTASVGLFLTAIARYISIHRLPLAYKRIIVTRPKAVAFCLM	240
Db	181	HRKDSRNVLFLKGGVTASTASVGLFLTAIARYISIHRLPLAYKRIIVTRPKAVAFCLM	240
QY	241	WTIAIVAVLPVLGNCKEKLQSCVDIFPHIDTYLMFWIGVTSVLLLFIVVAYMYILWK	300
Db	241	WTIAIVAVLPVLGNCKEKLQSCVDIFPHIDTYLMFWIGVTSVLLLFIVVAYMYILWK	300
QY	301	AHSHAVRMIQRTQKSIITHTSDEGKVQVTRPDQARMAIRLAKTLVLVLICWGPLL	360
Db	301	AHSHAVRMIQRTQKSIITHTSDEGKVQVTRPDQARMDIRLAKTLVLVLICWGPLL	360
QY	361	AIMVYDVGKWNKLIKTVPFAPCSMLCLLNSTVNPITIIYALRSKDLRHAFRSPSCGTAQ	420
Db	361	AIMVYDVGKWNKLIKTVPFAPCSMLCLLNSTVNPITIIYALRSKDLRHAFRSPSCGTAQ	420
QY	421	PLDNSMGDSCLHKKHANNAAVHRAAESCIKSTVKIAKVTMSVTDTSAEAL	472
Db	421	PLDNSMGDSCLHKKHANNAAVHRAAESCIKSTVKIAKVTMSVTDTSAEAL	472
- RESULT 2			
A33117			
cannabinoid receptor CB1 - rat			
C;Species: Rattus norvegicus (Norway rat)			
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004			
C;Accession: A33117; C55879			
R;Matuoda, L.A.; Lolait, S.J.; Brownstein, M.J.; Young, A.C.; Bonner, T.I.			
Nature 346, 561-564, 1990			
A;Title: Structure of a cannabinoid receptor and functional expression of the cloned cDN			
A;Reference number: A33117; MUID:90332039; PMID:2165569			
A;Accession: A33117			
A;Molecule type: mRNA			
A;Residues: 1-473 <SHI>			
A;Cross-references: UNIPROT:P20272; UNIPARC:UPI000012710C; GB:X55812; NID:G1552375; PIDN			
R;Shire, D.; Carillon, C.; Kaghad, M.; Calandra, B.; Rinaldi-Carmona, M.; Le Fur, G.; Ca			
J. Biol. Chem. 270, 3726-3731, 1995			
A;Title: An amino-terminal variant of the central cannabinoid receptor resulting from al			
A;Reference number: A55879; MUID:95181329; PMID:7876112			
A;Accession: C55879			
A;Status: preliminary; not compared with conceptual translation			
A;Molecule type: mRNA			
A;Residues: 1-107 <SHI>			
A;Cross-references: UNIPARC:UPI000017C808			
C;Keywords: G protein-coupled receptor; glycoprotein; membrane protein			
Query Match 96.7%; Score 2343.5; DB 2; Length 473;			
Best Local Similarity 96.8%; Pred. No. 3.7e-186;			
Matches 458; Conservative 5; Mismatches 9; Indels 1; Gaps 1;			
QY	1	MKSILDGLADTTTTRTTITDLYYGSNDIQYEDIKGDMAKGLGYFPQKFLTSPRGSPFOE	60
Db	1	MKSILDGLADTTTTRTTITDLYYGSNDIQYEDIKGDMAKGLGYFPQKFLTSPRGSPFOE	60
QY	61	KMTAGNPOLVPA-DQVNITEFNKLSLSPKENEENIQCGENPMDIECFWVLPNSQQALAI	119
Db	61	KMTAGNPLVPAGDTTNTITEFNKLSLSPKENEENIQCGENPMDIECFWVLPNSQQALAI	120
QY	120	AVLSLTGTFTVLENLLVLCVILHSRLCRPSYHFTIGSLAVADLLGSVIFVYSFIDFHFV	179
Db	121	AVLSLTGTFTVLENLLVLCVILHSRLCRPSYHFTIGSLAVADLLGSVIFVYSFIDFHFV	180
QY	180	FHRKDSRNVLFLKGGVTASTASVGLFLTAIARYISIHRLPLAYKRIIVTRPKAVAFCL	239

Db	181	FHRKDSRNVLFLKGGVTASTASVGLFLTAIARYISIHRLPLAYKRIIVTRPKAVAFCL	240
QY	240	MWTIAIVAVLPVLGNCKEKLQSCVDIFPHIDTYLMFWIGVTSVLLLFIVVAYMYILW	299
Db	241	MWTIAIVAVLPVLGNCKEKLQSCVDIFPHIDTYLMFWIGVTSVLLLFIVVAYMYILW	300
QY	300	KAHSHAVRMIQRTQKSIITHTSDEGKVQVTRPDQARMAIRLAKTLVLVLICWGPLL	359
Db	301	KAHSHAVRMIQRTQKSIITHTSDEGKVQVTRPDQARMDIRLAKTLVLVLICWGPLL	360
QY	360	LAIMVYDVGKWNKLIKTVPFAPCSMLCLLNSTVNPITIIYALRSKDLRHAFRSPSCGTA	419
Db	361	LAIMVYDVGKWNKLIKTVPFAPCSMLCLLNSTVNPITIIYALRSKDLRHAFRSPSCGTA	420
QY	420	QPLDNSMGDSCLHKKHANNAAVHRAAESCIKSTVKIAKVTMSVTDTSAEAL	472
Db	421	QPLDNSMGDSCLHKKHANNAAVHRAAESCIKSTVKIAKVTMSVTDTSAEAL	473
RESULT 3			
S70364			
cannabinoid receptor CB2, peripheral - mouse			
N;Alternate names: G protein-coupled receptor CB2			
C;Species: Mus musculus (house mouse)			
C;Date: 21-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004			
C;Accession: S70364; S54163			
R;Shire, D.; Calandra, B.; Rinaldi-Carmona, M.; Oustric, D.; Pessague, B.; Bonnin-Caban			
Biochim. Biophys. Acta 1307, 132-136, 1996			
A;Title: Molecular cloning, expression and function of the murine CB2 peripheral cannab			
A;Reference number: S70364; MUID:96283804; PMID:8679694			
A;Accession: S70364			
A;Molecule type: mRNA			
A;Residues: 1-347 <SHI>			
A;Cross-references: UNIPROT:P47936; UNIPARC:UPI00000019CE; EMBL:X86405; NID:G791081; PFI			
C;Superfamily: melanocortin receptor			
C;Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein			
Query Match 30.3%; Score 734.5; DB 2; Length 347;			
Best Local Similarity 48.2%; Pred. No. 3.8e-53;			
Matches 150; Conservative 53; Mismatches 89; Indels 19; Gaps 4;			
QY	99	GENFMDIECFWVLPNSQQALAIASLTGLTFTVLENLLVLCVILHSRLCRPSYHFI	158
Db	16	GLEFNPMEKYMILSSQQIAVAVLCTLMGLLSALENMAVLYILSRRLRRKPSYLI	75
QY	159	LAVADLLGSVIFVYSFIDFHFVRKDSRNVLFLKGGVTASTASVGLFLTAIARYISI	218
Db	76	LADADFLASVIFACNFVIFVHFGVDSNAIFLLKIGSVTMTFTASVGSLLLTAVDRYLCL	135
QY	219	HRPLAYKRIIVTRPKAVAFCLMWTIAIVAVLPVLGNCKEKLQSCVDIFPHIDTYLMF	278
Db	136	CYPTPYKALVTRGRALVLCVMVLSALISYPLMGWTC--CPSPCELSFLIPNDYLLG	193
QY	279	WIGVTSVLLLFIVVAYMYILWKAHSHAVRMIQRTQKSIITHTSDEGKVQVTRPDQARMA	338
Db	194	WLLFTAILFGIITVYGVVWKAHRHVAATLAEH-----QDRQV----PGIARMR	238
QY	339	--IRLAKTLVLVLICWGPLLAIWYDVGKWNKLIKTVPFAPCSMLCLLNSTVNP	396
Db	239	LDVRLAKTLGLVLVLLICWFPFALALMGHSLVTLTSDQVKEAFAPCSMLCLVNSM	298
QY	397	YALRSKDLRHA 407	
Db	299	YALRSGEIRSA 309	
RESULT 4			
S36750			
cannabinoid receptor CB2 - human			
N;Alternate names: cannabinoid receptor, peripheral			
C;Species: Homo sapiens (man)			
C;Date: 22-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999			


```
RESULT 7
JC7559
sphingosine 1-phosphate receptor - zebra fish
N/Alternate names: endothelial differentiation gene 1 receptor
C:Species: Brachydanio rerio (zebra fish)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C:Accession: JC7559
R:Im, D.S.; Ungar, A.R.; Lynch, K.R.
Biochem. Biophys. Res. Commun. 279, 139-143, 2000
A:Title: Characterization of a zebrafish (Danio rerio) sphingosine 1-phosphate receptor
A:Reference number: JC7559; MUID: 20563813; PMID:11112429
A:Accession: JC7559
A:Molecule type: DNA
A:Residues: 1-362 <TMA>
A:Cross-references: UNIPROT:Q9DDK4; UNIPARC:UPI00001788F3; GB:AF321294
C:Comment: This receptor, a G protein-coupled receptor, mediates sphingosine 1-phosphate
or also functions in the developing central nervous system in cell proliferation, apopto
C:Genetics:
A:Gene: edg1
C:Superfamily: G protein-coupled receptor edg-1
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 14.4%; Score 348.5; DB 2; Length 362;
Best Local Similarity 27.9%; Pred. No. 3.6e-21;
Matches 102; Conservative 69; Mismatches 129; Indels 65; Gaps 13;

QY 118 ATAVLSLTGTFVLENLVLCVILHSRLCRPSYHFGSLAVADLLGSLVIFVYSFIDF 177
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 26 ADSWPFIVCCFTILENLVLLTWTWKPH-KPMYYFIGNLALSOLLGAVVYTNILLS 84

QY 178 HVFHRKDSRVNLFVLGGVTSFTASVGSFLTAIARIYSIHRPLAYKRVTRPKAVAF 237
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 85 GANTYKLTPTQFFREGSMFVALAASVFLAIAIERHILTMLK----MKLHNKTKRVF 140

QY 238 CL---MWTIAIVAPLPLGWNCEKLSQVCSDFPHIDETFLMFWIGVTSVLLLFIV--Y 292
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 141 MLISTWFWIAALGGLPVGWNCIDSNCTVLPYKAYILFCVTFPSVILMAIVILY 200

QY 293 AYMYILWKAHSHAV--RMIQ--RGTKSIIHTSEDGKQVQVTRPDQARMAIRLAKTLVL 348
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 201 ARYALVTRTSRKLVRKVGANGSGNSK-----ACQYL--TCSILYKAEWFLALAVINSANPLIYTL 242

QY 349 LVVLIICWGPLLAIMVYDFGKMNKLIKTVAFCSM-----LCLLNSTVNPPIYAL 399
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 243 LSCFIACWAPLFILLILDV-----ACQYL--TCSILYKAEWFLALAVINSANPLIYTL 294

QY 400 RSKDLRHAFRSMPPSCGTAQP-----LDNSMGDSCLHKKHANNAAASVHRAAE 447
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 295 TSNEMRRAFTKML-NCGVCVQPSGKFSRPIMGAEFSTKSDNS---SHPNKDEPEYSRE 350

QY 448 SCIKS 452
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 351 TIVSS 355

RESULT 8
JC5245
G protein-coupled receptor - human
C:Species: Homo sapiens (man)
C:Date: 13-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: JC5245
R:Yamaguchi, F.; Tokuda, M.; Hatase, O.; Brenner, S.
Biochem. Biophys. Res. Commun. 227, 608-614, 1996
A:Title: Molecular cloning of the novel human G protein-coupled receptor (GPCR) gene map
A:Reference number: JC5245; MUID:97032811; PMID:8878560
A:Accession: JC5245
A:Molecule type: DNA
A:Residues: 1-378 <YAM>
A:Cross-references: UNIPROT:Q99500; UNIPARC:UPI0000050422; EMBL:X83864; NID:g1770395; PI
C:Comment: This protein transduces hormone and neurotransmitter signals into intracellul
C:Genetics:
A:Gene: edg-3
```

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A:Map position: 9q22.1-q22.2
C:Superfamily: G protein-coupled receptor edg-1
C:Keywords: G protein-coupled receptor

Query Match 14.3%; Score 346.5; DB 2; Length 378;
Best Local Similarity 29.4%; Pred. No. 5.5e-21;
Matches 104; Conservative 61; Mismatches 132; Indels 57; Gaps 13;

QY 121 VLSLTGTFVLENLVLCVILHSRLCRPSYHFGSLAVADLLGSLVIFVYSFIDFHV 180
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 44 VLFLVICSFIVLENLVLAIAWKNKFNHR-MYFFIGNLALCDLLAGIAYKNIL---MS 99

QY 181 HRKD---SRNVFLFKGGVTSFTASVGSFLTAIARIYSI--HRPL-AYKRVTRPKAV 234
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 100 GKTKTSLSPVWFLREGSMFVALGASTCSLLAIAIERHILTMKRPYDANKR--HRVFL 157

QY 235 VAFCLMWTIAIVAPLPLGWNCEKLSQVCSDFPHIDETFLMFWIGVTSVLLLFIV--Y 292
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 158 IGMC--WLTAFTLIGALPILGWNCLHNLPCDCTILPLYSKKYIAFCISIFAILVTIVILY 215

QY 293 AYMYILWKAHSHAVRMIOGRGTSIIHTSEDGKQVQVTRPDQARMAIRLAKTLVLVL 352
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 216 ARIYFLVKSSR-----KVANNNSERSMALLRTVIVVVSVP 252

QY 353 IICWGPLLAIMVYDFGKMNK---LIKTVAFCSMLCLNNTVNPPIIYALRSKDLRHAF 409
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 253 IACMSPLFLFLIDVACRVQACPIFLKQWFI--VLAVLNSAMNPVIYTLASKEMRRAPF 310

QY 410 SNFPSC-----EGTAQPLDNSMGDSCLHKKHANNAAAS-----VHRAAESCI 450
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 311 RLVCNCLVRGRGARASPIQALDPDSRSSSSSSSSSHSPKVEDLPHTDPSSCI 364

RESULT 9
I53870
Edg-1 orphan receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C:Accession: I53870
R:Lado, D.C.; Browe, C.S.; Gaskin, A.A.; Borden, J.M.; MacLennan, A.J.
Gene 149, 331-336, 1994
A:Title: Cloning of the rat edg-1 immediate-early gene: expression pattern suggests div
A:Reference number: I53870; MUID:95047498; PMID:7959012
A:Accession: I53870
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-383 <RES>
A:Cross-references: UNIPROT:P48303; UNIPARC:UPI0000129BD0; EMBL:U10303; NID:g959396; PI
C:Superfamily: G protein-coupled receptor edg-1

Query Match 14.0%; Score 340; DB 2; Length 383;
Best Local Similarity 28.3%; Pred. No. 1.9e-20;
Matches 95; Conservative 62; Mismatches 123; Indels 56; Gaps 9;

QY 120 AVLSLTGTFVLENLVLCVILHSRLCRPSYHFGSLAVADLLGSLVIFVYSFIDFHV 179
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 50 SVVFILICLLIILENIFVLLTIWTKKPH-RPMYTFIGNLALSOLLGAVAYTANLLLSGA 108

QY 180 FHRKDSRVNLFVLGGVTSFTASVGSFLTAIARIYSI--HRPLAYKRVTRPKAVAF 238
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 109 TTYKLTTPAQWFLREGSMFVALSASFSLAIAIERYITMLKWLKLNHNGSSSSRFLISAC 168

QY 239 LMWTIAIVAPLPLGWNCEKLSQVCSDFPHIDETFLMFWIGVTSVLLLFIV--YAYMY 296
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 169 --WVLSLILGGPIGWNCISLSSCSTVLPYHKHYILFCTVTFVLLLSIVILYCRY 226

QY 297 ILWKAHSHA-----VRMIQRTGQKSI--IHTSEDGKQVQVTRPDQARMAIRLAKTLVL 350
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 227 SLVTRSRRLTRFKNKISKASRSSEKS-----LALLKTVILVS 264

QY 351 VLIIICWGPLLAIMVYDFGKMNKLIKTVF--AFCSMLCLNNTVNPPIIYALRSKDLRHAF 408
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 265 VFIACWAPLFILLILDV-GCKAKTCDILYKASYFLVLAVINSGTNPPIIYTLTKEMRRAP 323
```

Qy 409 -----BSMFPSCRGTAQPLDMS 425
Db 324 IRIISCKCPNGDSAGKPKPIIPGMBFSPKSDNS 359

RESULT 10

alpha-1A adrenergic receptor - Japanese medaka
C;Species: Oryzias latipes (Japanese medaka)
C;Date: 23-Jul-1997 #sequence_revision 01-Aug-1997 #text_change 17-Mar-1999
C;Accession: S71323
Eur J. Biochem. 235, 501-507, 1996
R;Yasuoka, A.; Abe, K.; Arai, S.; Emori, Y.
A;Title: Molecular cloning and functional expression of the alpha-1-A-adrenoceptor of Me
A;Reference number: S71323; MUID:96184522; PMID:8654394
A;Accession: S71323
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-477 <VAS>
A;Cross-references: UNIPARC:UPI00001778AD; EMBL:D63859
A;Note: it is uncertain whether Met-1 or Met-8 is the initiator
C;Superfamily: vertebrate rhodopsin

Query Match 12.6%; Score 306.5; DB 2; Length 477;
Best Local Similarity 27.4%; Pred. No. 1.5e-17;
Matches 93; Conservative 69; Mismatches 130; Indels 47; Gaps 13;

Qy 107 CFMVLNPS-QQLAIAVLSLTIGTFT---VLENLLVLCVILHSRLCRPSYHFTGSLAVA 162
Db 20 CSHVLAPELNTKAVVLGMVLGIFLFGVIGNILVILSVCHRHQ-TVTYFYVNLAVA 78
Qy 163 D-LLGSVTFVYSFIDFVHFRKDRNVFLFKGGV-TASFTASVGSFLTAIARYSIHR 220
Db 79 DLLLSSTVLPSSAI-FEILDRWFRGVFCNIWAAVDVLCCTASIMSLCVISVDRYIGVS 137
Qy 221 PLAYKRIVTRPKAVAFCLMTIAIVAVLPGLGN---CEKLSQVCS-----DIPPHI 271
Db 138 PLRYPALMTKRRALLAVMLLVLSIIGLFGWKEPAPDETVCKITEPFGVAIPSAV 197
Qy 272 DETYLMFWIGVTSVLLLFIVYAYMYILWKAHSHAVR---MIQRTQKSIHH-----T 321
Db 198 GSFYL-----PLAILAMCYRVVVAQESRGLKEQKIEKSDSEQVILRMHGRNTV 250
Qy 322 SEDGKVQVTRPDQARMAIRL-----AKTLVLVLVLIICWGPLLAIMVYDFGKWN 372
Db 251 SEDEALR----SRTHFALRLKLSGREKKAATLGIWVGCFLVCLWLPFLVLPFGSIIPAY 306
Qy 373 KLIKTVPFCSMLCLNSTVNPPIIYALRSKDLRHAFRSM 411
Db 307 RPSDTVFKITPWLGVFNSCINPIIYLCNSQBFKKAQSL 345

RESULT 11

JC2193
melanocortin receptor, MC5 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004
C;Accession: JC2193
R;Griffon, N.; Mignon, V.; Facchinetti, P.; Diaz, J.; Schwartz, J.C.; Sokoloff, P.
Biochem. Biophys. Res. Commun. 200, 1007-1014, 1994
A;Title: Molecular cloning and characterization of the rat fifth melanocortin receptor.
A;Reference number: JC2193; MUID:94234987; PMID:8179577
A;Accession: JC2193
A;Molecule type: DNA
A;Residues: 1-325 <GRI>
A;Cross-references: UNIPROT:P35345; UNIPARC:UPI000012ED53; GB:L27081; NID:9435606; PIDN:
C;Superfamily: melanocortin receptor
C;Keywords: G protein-coupled receptor; receptor; transmembrane protein
F;37-63/Domain: transmembrane #status predicted <TM1>
F;73-98/Domain: transmembrane #status predicted <TM2>
F;117-138/Domain: transmembrane #status predicted <TM3>
F;159-179/Domain: transmembrane #status predicted <TM4>

F;193-211/Domain: transmembrane #status predicted <TM5>
F;240-263/Domain: transmembrane #status predicted <TM6>
F;276-297/Domain: transmembrane #status predicted <TM7>

Query Match 12.6%; Score 305; DB 2; Length 325;
Best Local Similarity 27.5%; Pred. No. 1.2e-17;
Matches 95; Conservative 66; Mismatches 118; Indels 66; Gaps 13;

Qy 92 NEENIQGEMFMDIECFMVLNPS---QQLAIAV-LSLTIGTFTVLENLLVLCVILHSRL 147
Db 17 SEDNI-LGQN-----VNNKSSACEDMGIAVEFTLGLSVLEENILVIGAVKKNL 67
Qy 148 RCRPSYHFIGSLAVADLLGSVIFYYSIDFVHFRKD--SRNVPLFKGGV-----TASP 200
Db 68 H-SMWYFFVGSGLAVADMLVSMNSNAWETITIVLINNHVIAADTFVRHIDNVFDSMICISV 126
Qy 201 TASVGSFLTAIARYSIHRPLAYKRIVTRPKAVAFCLMTIAIVAVLPGLGNCEKL 260
Db 127 VASMSLLAIAVDRIYITIFVALRYHHIMTARRSGVIIACIWTFCISGIVFIPIIYE-SKY 185
Qy 261 QSVCSDFPHIDETVLMFWIGVTSVLLLFIVYAYMYILWKAHSHAVRMIQRTQKSIHH 320
Db 186 VIVC-----LISMPFTMLFFWVSLYIHFLLARNHVKRIASPRNSV--- 228
Qy 321 TSEDGKVQVTRPDQARMAIRLAKTLVLVLVLIICWGPLLAIMVYDFGKKNLIKTVFA 380
Db 229 -----RQRASMKGAITLTMGLGIFVCSPPFLHLILMISCPQN-----VYC 270
Qy 381 FCSM-----LCLNSTVNPPIIYALRSKDLRHAFRSMFPSCG 417
Db 271 ACFSYFNMYLLILMCSNVIDPLIYALRSQEMRTFKKII-CCHG 314

RESULT 12

149008
melanocortin-5 receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 149008; A54245; JC2244
R;Pathi, Z.; Iben, L.G.; Parker, E.M.
Neurochem. Res. 20, 107-113, 1995
A;Title: Cloning, expression, and tissue distribution of a fifth melanocortin receptor
A;Reference number: 149008; MUID:95258173; PMID:7739752
A;Accession: 149008
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-372 <RSS>
A;Cross-references: UNIPROT:P41149; UNIPARC:UPI000016384D; EMBL:U08354; NID:9522165; P:
R;Labbe, O.; Desarnaud, P.; Eggerickx, D.; Vassart, G.; Parmentier, M.
Biochemistry 33, 4543-4549, 1994
A;Title: Molecular cloning of a mouse melanocortin 5 receptor gene widely expressed in
A;Reference number: A54245; MUID:94213827; PMID:8161509
A;Accession: A54245
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 48-120, 'P', 122-372 <LAB>
A;Cross-references: UNIPARC:UPI000027516; GB:X76295; NID:9498973; PIDN:CAA53943.1; P:
A;Experimental source: Clone HGMPO1B
A;Note: sequence extracted from NCBI backbone (NCBIP:145988)
R;Gantz, I.; Shimoto, Y.; Konda, Y.; Miwa, H.; Dickinson, C.J.; Yamada, T.
Biochem. Biophys. Res. Commun. 200, 1214-1220, 1994
A;Title: Molecular cloning, expression, and characterization of a fifth melanocortin r.
A;Reference number: JC2244; MUID:94241974; PMID:8185570
A;Accession: JC2244
A;Molecule type: DNA
A;Residues: 48-372 <GAN>
A;Cross-references: UNIPARC:UPI0000147322; GB:L22527; NID:9468377; PIDN:AAA21337.1; P:
C;Comment: This protein responds to melanocortins with an increase in intracellular c
C;Superfamily: melanocortin receptor
C;Keywords: receptor; transmembrane protein
F;84-109/Domain: transmembrane #status predicted <TM1>
F;121-144/Domain: transmembrane #status predicted <TM2>
F;164-185/Domain: transmembrane #status predicted <TM3>

F:206-226/Domain: transmembrane #status predicted <TM4>
F:232-257/Domain: transmembrane #status predicted <TM5>
F:287-310/Domain: transmembrane #status predicted <TM6>
F:324-344/Domain: transmembrane #status predicted <TM7>

Query Match 12.5%; Score 304; DB 2; Length 372;
Best Local Similarity 26.4%; Pred. No. 1.8e-17;
Matches 84; Conservative 67; Mismatches 123; Indels 44; Gaps 9;

QY 115 QQLAIIV-LSLTGLTFTVLENLVLCVILHSRLCRPSYHFGSLAVADLLGSLVIFYYS 173
DB 81 EEMGIAVEVFLTLGLVSLLENILVIGAIYKKNLH-SPMYFYVGSVAVADMLVMSNAWE 139

QY 174 FIDFVHFHKKD--SRNVFLFKGV-----TASFTASVGLFTATARIYISIHRLPLAYKR 226
DB 140 TTVIYLNNKHLVIADTFVRHIDNVFDSMICISVASMCSLLAIAVDRIITIFALRYHH 199

QY 227 IVTRPKAVVAFCLMWTIAIVLPLLGWNCCKLQVSCSDIPPHIDETVLMFWMIGVTSVL 286
DB 200 IMTARSGVLIACIWTFCISGVFIYYE-SKYVIIC-----LISMFFTM 244

QY 287 LFLFIYVAYVYLWKASHAVRMQRTQKSIHTSEDGKQVQVTRPDQARMAIRLAKTLV 346
DB 245 LFFMWSLYTHMFLAARNHVKRIIAASPRYNSVRQRTSMKGA-----TLT 288

QY 347 LILVLVLIICWGPLLAIIMVDFVFGKMKLIKTVFAFCSM---LCLNLTWNPIIYALRSKD 403
DB 289 MLLGIFIVCWSPFHLILMISCPQNYCSPMSYFNWVLLIMCNSVIDPLIYALRSQE 348

QY 404 LRHAFRSMPPSCBGTAPQ 421
DB 349 MRRTFKEIV-CHGFRPP 365

RESULT 13
JC1465
Probable G protein-coupled receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: JC1465
R:Okazaki, H.; Ishizaka, N.; Sakurai, T.; Kurokawa, K.; Goto, K.; Kumada, M.; Takuwa, Y.
Biochem. Biophys. Res. Commun. 190, 1104-1109, 1993
A:Title: Molecular cloning of a novel putative G protein-coupled receptor expressed in b
A:Reference number: JC1465; MUID:93176155; PMID:8382486
A:Accession: JC1465
A:Molecule type: mRNA
A:Residues: 1-352 <OKA>
A:Cross-references: UNIPROT:P47752; UNIPARC:UPT000000007D; GB:AB016931; NID:g3445557; PT
A:Experimental source: aortic smooth muscle
C:Superfamily: G protein-coupled receptor edg-1
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot
F:35-59/Domain: transmembrane #status predicted <TM1>
F:67-95/Domain: transmembrane #status predicted <TM2>
F:110-128/Domain: transmembrane #status predicted <TM3>
F:148-173/Domain: transmembrane #status predicted <TM4>
F:190-210/Domain: transmembrane #status predicted <TM5>
F:224-255/Domain: transmembrane #status predicted <TM6>
F:272-293/Domain: transmembrane #status predicted <TM7>
F:19/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:142,145,218,219,329,330,332/Binding site: phosphate (Ser) (covalent) #status predi
F:313/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 12.2%; Score 296.5; DB 2; Length 352;
Best Local Similarity 29.4%; Pred. No. 6.9e-17;
Matches 99; Conservative 48; Mismatches 117; Indels 73; Gaps 12;

QY 92 NEENIQCGENFMDIECFMVLNPNSQLAIAVLSLTGLTFTVLENLVLCVILHSRLCRP 151
DB 10 NPEKVQEHYNYTKETLDMQETPSRKVASAFI-IILCCAIWVENLVLIIVARNSEKH-SA 67

QY 152 SYHPIGSLAVADLLGSLVIFY-----YSFIDFVHFHKKDSRVNVLFLKGGVTSFT 201
DB 68 MYLFLGNLAASDLLAGVAFVNTLLSGPVLTSLTLQWFARE-----GSAPITLIS 117

QY 202 ASVGSGLFTATARIYISIHRLPLAYKRIVTRPKAVVAFCLM---WTIAIVLAVLPLLGWNC 258
DB 118 ASVFSLLAIAIERQVAI---AKVKLYGSDKSCRMMLIGASWLSLILGGLPILGWNC 173

QY 259 KIQSVCSIDIPPHIDETVLMFWMIGVTSVLLLFVIVAYMYLWKAH-SHAVRMQRTQKSI 317
DB 174 DHLEACSTVPLIYAKHYVLCVVITFISVILLAIVALYVRIYFVVRSSHA----- 221

QY 318 IIHTSEDGKQVQVTRPDQARMAIRLAKTLVLIWLVLIICWGPLLAIIMVDF-VP 368
DB 222 -----DVAGP-----QTLALKTKTVILGVFIICWLPAPFASILLDSTCPVRACPV 267

QY 369 GRMNKLIKTVFAFCSMCLNLTWNPIIYALRSKDLR 405
DB 268 YKAHYF-----FAFAT-----LNSLLNPVIYTWESRDLR 296

RESULT 14
S40454
G protein-coupled receptor GPCR21 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S40454
R:Saeki, Y.; Ueno, S.; Mizuno, R.; Nishimura, T.; Fujimura, H.; Nagai, Y.; Yanagihara, H.
FEBS Lett. 336, 317-322, 1993
A:Title: Molecular cloning of a novel putative G protein-coupled receptor (GPCR21) whic
A:Reference number: S40454; MUID:94085630; PMID:8262253
A:Accession: S40454
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-330 <SAE>
A:Cross-references: UNIPROT:P35413; UNIPARC:UPI0000025C17; GB:D21062; NID:g455487; PIDN
C:Superfamily: melanocortin receptor
C:Keywords: G protein-coupled receptor; phosphoprotein; transmembrane protein

Query Match 12.2%; Score 295.5; DB 2; Length 330;
Best Local Similarity 28.0%; Pred. No. 7.8e-17;
Matches 90; Conservative 61; Mismatches 125; Indels 45; Gaps 13;

QY 111 LNPSQLAIAVLSLTGLTFTVLENLVLCVILHSRLCRPSYHFGSLAVADLLGSLVIF 170
DB 36 LLPSPRAMDVLCIS-GTLVSCENALVVAIIVGTFAFRA-PMFLVGSVAVADLLAGL 93

QY 171 VYYSF-IDFVHFHKKDSRVNVLFLKGGVTSFTASVGSGLFTATARIYISIHRLPLAYKRIVT 229
DB 94 VLHFAADFCL-----GSPENSLMVLGVLAWAFASIGSLLAITVDRLSYLNALTYVSETT 149

QY 230 RPKAVVAFCLMWTIAIVLPLLGWNCCKLQVSCSDIPPHIDETVLMFWMIGVTSVLLIF 289
DB 150 VTRTTYMLALVWVGALGLVPLAWNCRDGLTTCGVVYP-LSKNHL-----VVLAIAPF 203

QY 290 IYVAYMYLWKASHAVRMQRTQK-SIIHTSEDGKQVQVTRPDQARMAIRLAKTLVLI 348
DB 204 MVFG-----IMQLYQAQICRIVCRHAQOIALQRLLPASHVAVTRKGI-----TLAVV 252

QY 349 LVVLIICWGPLLAIIMVDFVFGKMKLIKTVFAFCSM-LCLNLTWNPIIYALRSKDLRHA 407
DB 253 LGAPACW---LPFTVYCLLGADS---PRLYTYLTLLPATYNSMINPVIYAFENQDVQKV 307

QY 408 -----FRSMFPPS 414
DB 308 LWAICCCSTSKIPFRSRSPS 328

RESULT 15
I46416
melanocyte-stimulating hormone receptor - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C>Date: 19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change 09-Jul-2004
C:Accession: I46416; S43120
R:Barrett, P.; MacDonald, A.; Helliwell, R.; Davidson, G.; Morgan, P.
J. Mol. Endocrinol. 12, 203-213, 1994

A;Title: Cloning and expression of a new member of the melanocyte-stimulating hormone re
A;Reference number: I46416; MUID:94338523; PMID:8060485
A;Accession: I46416
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-325 <BAR>
A;Cross-references: UNIPROT:P41983; UNIPARC:UPI000012ED54; EMBL:Z31369; NID:9467692; PID
A;Note: submitted to the EMBL Data Library, March 1994
C;Superfamily: melanocortin receptor

Query Match		12.0%; Score 292; DB 2; Length 325;
Best Local Similarity		28.4%; Pred. No. 1.5e-16;
Matches		99; Conservative 61; Mismatches 88; Indels 100; Gaps 17;
Qy	112	NPSQQLAIIV-LSLTIGTFTVLENLVLCVILHSRSLRCPSPYHFGISLAVADLLGSV-- 168
Db	31	SPCEDMGIAVEVFLALGLISLLENILVIGAIVRNRNIHI-PMYFFVGSLAVADMLVSLN 89
Qy	169	----IFVYSFIDFHVPHRKDS----RNVFLKLGGVTFASVGSISLFLTAIARYISIH 220
Db	90	FWETIYIYLLTNKHLVWADASVRHLDNVP---DSMICISVVASMCSLAIADVRYTIFC 146
Qy	221	PLAYKRIVT--RPKAVV---AFCLMWTIAIVIAVLPLGWNCKEKLQSVCSDFP-PHIDE 273
Db	147	RLAYQRIMTGRSGAIIAGIWAFC-----TSCGTVFIVVYES 183
Qy	274	TYL-----MFWIGVTSVLLFIVYAYMYILWKAHSHAVRMIOGTOKSIIHTSEDKV 327
Db	184	TYVVVCLIAMF--LTMLLMASLYTHMFLARTH---VRR-----AALPGHSSV--- 228
Qy	328	QVTRPDQARMAIRLAKTLVLILVLLICWGPLLAIMVYDVFGKMKLIKTVFAFCS--- 383
Db	229	-----KQRTGVKGAITLMLLGVFLICWAPFFLHLILMISCPQN-----LYCSCFMS 275
Qy	384	-----MLCLLNSTVNPPIIYALRSKOLRHAFRSM-----PPS 414
Db	276	HNNYLLIMCNSVIDPLIYAFRSQEMKTKFKEIVCFQGFRTPCRPFS 323

Search completed: January 6, 2006, 21:14:03
Job time : 42 secs

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